FIG. 1A

```
1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60

61 TGCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120

121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180

181 AGGCCTGAAG GAACAGGCCG GGGAAGGAGC CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240

241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
  1                          M  A  R  A  H  W  G  C  C  P  W  L  12

301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V  L  L  C  A  C  A  W  G  H  T  K  P  L  D  L  G  G  Q  D  32

361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V  R  N  C  S  T  N  P  P  Y  L  P  V  T  V  V  N  T  T  M  52

421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S  L  T  A  L  R  Q  Q  M  Q  T  Q  N  L  S  A  Y  I  I  P  72

481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G  T  D  A  H  M  N  E  Y  I  G  Q  H  D  E  R  R  A  W  I  92

541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T  G  F  T  G  S  A  G  T  A  V  V  T  M  K  K  A  A  V  W  112

601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
113 T  D  S  R  Y  W  T  Q  A  E  R  Q  M  D  C  N  W  E  L  H  132

661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
133 K  E  V  G  T  T  P  I  V  T  W  L  L  T  E  I  P  A  G  G  152

721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
153 R  V  G  F  D  P  F  L  L  S  I  D  T  W  E  S  Y  D  L  A  172

781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
173 L  Q  G  S  N  R  Q  L  V  S  I  T  T  N  L  V  D  L  V  W  192

841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
193 G  S  E  R  P  P  V  P  N  Q  P  I  Y  A  L  Q  E  A  F  T  212

901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
213 G  S  T  W  Q  E  K  V  S  G  V  R  S  Q  M  Q  K  H  Q  K  232
```

FIG. 1B

```
 961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V  P  T  A  V  L  L  S  A  L  E  E  T  A  W  L  F  N  L  R  252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A  S  D  I  P  Y  N  P  F  F  Y  S  Y  T  L  L  T  D  S  S  272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
 273 I  R  L  F  A  N  K  S  R  F  S  S  E  T  L  S  Y  L  N  S  292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S  C  T  G  P  M  C  V  Q  I  E  D  Y  S  Q  V  R  D  S  I  312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q  A  Y  S  L  G  D  V  R  I  W  I  G  T  S  Y  T  M  Y  G  332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I  Y  E  M  I  P  R  E  K  L  V  T  D  T  Y  S  P  V  M  M  352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
 353 T  K  A  V  K  N  S  K  E  Q  A  L  L  K  A  S  H  V  R  D  372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A  V  A  V  I  R  Y  L  V  W  L  E  K  N  V  P  K  G  T  V  392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
 393 D  E  F  S  G  A  E  I  V  D  K  F  R  G  E  E  Q  F  S  S  412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G  P  S  F  E  T  I  S  A  S  G  L  N  A  A  L  A  H  Y  S  432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P  T  K  E  L  N  R  K  L  S  S  D  E  M  Y  L  L  D  S  G  452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
 453 G  Q  Y  W  D  G  T  T  D  I  T  R  T  V  H  W  G  T  P  S  472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A  F  Q  K  E  A  Y  T  R  V  L  I  G  N  I  D  L  S  R  L  492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I  F  P  A  A  T  S  G  R  M  V  E  A  F  A  R  R  A  L  W  512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D  A  G  L  N  Y  G  H  G  T  G  H  G  I  G  N  F  L  C  V  532
```

FIG. 1C

```
1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H  E  W  P   V  G  F   Q  S  N   N  I  A  M   A  K  G   M  F  T   552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S  I  E  P   G  Y  Y   K  D  G   E  F  G  I   R  L  E   D  V  A   572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L  V  V  E   A  K  T   K  Y  P   G  E  L  P   D  L  V   V  S  F   592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593 V  P  Y  D   R  N  L   I  D  V   S  L  L  S   P  E  H   L  Q  Y   612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L  N  R  Y   Y  Q  T   I  R  E   K  V  G  P   E  L  Q   R  R  Q   632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L  L  E  E   F  E  W   L  Q  Q   H  T  E  P   L  A  A   R  A  P   652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D  T  A  S   W  A  S   V  L  V   V  S  T  L   A  I  L   G  W  S   672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V  *                                                              673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940
```

FIG. 1D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428

FIG. 2A

```
  1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC  60

 61 TGCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120

121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180

181 AGGCCTGAAG GAACAGGCCG GGGAAGGAGC CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240

241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
  1                          M  A  R  A  H  W  G  C  C  P  W  L  12

301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V  L  L  C  A  C  A  W  G  H  T  K  P  L  D  L  G  G  Q  D  32

361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V  R  N  C  S  T  N  P  P  Y  L  P  V  T  V  V  N  T  T  M  52

421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S  L  T  A  L  R  Q  Q  M  Q  T  Q  N  L  S  A  Y  I  I  P  72

481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G  T  D  A  H  M  N  E  Y  I  G  Q  H  D  E  R  R  A  W  I  92

541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T  G  F  T  G  S  A  G  T  A  V  V  T  M  K  K  A  A  V  W  112

601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
113 T  D  S  R  Y  W  T  Q  A  E  R  Q  M  D  C  N  W  E  L  H  132

661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
133 K  E  V  G  T  T  P  I  V  T  W  L  L  T  E  I  P  A  G  G  152

721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
153 R  V  G  F  D  P  F  L  L  S  I  D  T  W  E  S  Y  D  L  A  172

781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
173 L  Q  G  S  N  R  Q  L  V  S  I  T  T  N  L  V  D  L  V  W  192

841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
193 G  S  E  R  P  P  V  P  N  Q  P  I  Y  A  L  Q  E  A  F  T  212

901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
213 G  S  T  W  Q  E  K  V  S  G  V  R  S  Q  M  Q  K  H  Q  K  232
```

FIG. 2B

```
961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V  P  T  A  V  L  L  S  A  L  E  E  T  A  W  L  F  N  L  R  252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
253 A  S  D  I  P  Y  N  P  F  F  Y  S  Y  T  L  L  T  D  S  S  272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
273 I  R  L  F  A  N  K  S  R  F  S  S  E  T  L  S  Y  L  N  S  292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
293 S  C  T  G  P  M  C  V  Q  I  E  D  Y  S  Q  V  R  D  S  I  312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q  A  Y  S  L  G  D  V  R  I  W  I  G  T  S  Y  T  M  Y  G  332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I  Y  E  M  I  P  R  E  K  L  V  T  D  T  Y  S  P  V  M  M  352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T  K  A  V  K  N  S  K  E  Q  A  L  L  K  A  S  H  V  R  D  372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A  V  A  V  I  R  Y  L  V  W  L  E  K  N  V  P  K  G  T  V  392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
393 D  E  F  S  G  A  E  I  V  D  K  F  R  G  E  E  Q  F  S  S  412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G  P  S  F  E  T  I  S  A  S  G  L  N  A  A  L  A  H  Y  S  432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
433 P  T  K  E  L  N  R  K  L  S  S  D  E  M  Y  L  L  D  S  G  452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
453 G  Q  Y  W  D  G  T  T  D  I  T  R  T  V  H  W  G  T  P  S  472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A  F  Q  K  E  A  Y  T  R  V  L  I  G  N  I  D  L  S  R  L  492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
493 I  F  P  A  A  T  S  G  R  M  V  E  A  F  A  R  R  A  L  W  512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D  A  G  L  N  Y  G  H  G  T  G  H  G  I  G  N  F  L  C  V  532
```

FIG. 2C

```
1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H  E  W  P   V  G  F   Q  S  N   N  I  A  M   A  K  G   M  F  T   552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S  I  E  P   G  Y  Y   K  D  G   E  F  G  I   R  L  E   D  V  A   572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L  V  V  E   A  K  T   K  Y  P   G  E  L  P   D  L  V   V  S  F   592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCGGAGCA TCTCCAGTAC 2100
 593 V  P  Y  D   R  N  L   I  D  V   S  L  L  S   P  E  H   L  Q  Y   612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L  N  R  Y   Y  Q  T   I  R  E   K  V  G  P   E  L  Q   R  R  Q   632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L  L  E  E   F  E  W   L  Q  Q   H  T  E  P   L  A  A   R  A  P   652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D  T  A  S   W  A  S   V  L  V   V  S  T  L   A  I  L   G  W  S   672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V  *                                                              673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940
```

FIG. 2D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428

FIG. 3A

```
 1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1       M  A  S  S  W  P  P  L  E  L  Q  S  S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  L  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  E  E  V  S  R  T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  R  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 3B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  R  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 4A

```
1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1       M  A  S  S  W  P  P  L  E  L  Q  S  S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  L  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  E  E  V  S  R  T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  R  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 4B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCAGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  Q  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 5A

```
 1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1       M  A  S  S  W  P  P  L  E  L  Q  S  S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCAA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  L  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  E  E  V  S  R  T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  R  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 5B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  R  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 6A

```
1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC 60
1 M  F  S  P  W  K  I  S  M  F  L  S  V  R  E  D  S  V  P  T  20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G  40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q  60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S  80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  V  L  L  L  F  I  280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

FIG. 6B

```
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
301 L  S  S  C   Q  D  E   R  I  I   D  V  I  T   Q  I  A   S  F  M   320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
321 A  Y  S  N   S  C  L   N  P  L   V  Y  V  I   V  G  K   R  F  R   340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K  K  S  W   E  V  Y   Q  G  V   C  Q  K  G   G  C  R   S  E  P   360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I  Q  M  E   N  S  M   G  T  L   R  T  S  I   S  V  E   R  Q  I   380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H  K  L  Q   D  W  A   G  S  R   Q  *                              391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

FIG. 6C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 6D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733

FIG. 7A

```
1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60

61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                               M  D  N  V  L  P  V  D  S  D  10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L  S  P  N  I  S  T  N  T  S  E  P  N  Q  F  V  Q  P  A  W  30

301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q  I  V  L  W  A  A  A  Y  T  V  I  V  V  T  S  V  V  G  N  50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V  V  V  M  W  I  I  L  A  H  K  R  M  R  T  V  T  N  Y  F  70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L  V  N  L  A  F  A  E  A  S  M  A  A  F  N  T  V  V  N  F  90

481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T  Y  A  V  H  N  E  W  Y  Y  G  L  F  Y  C  K  F  H  N  F  110

541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F  P  I  A  A  V  F  A  S  I  Y  S  M  T  A  V  A  F  D  R  130

601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y  M  A  I  I  H  P  L  Q  P  R  L  S  A  T  A  T  K  V  V  150

661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I  C  V  I  W  V  L  A  L  L  L  A  F  P  Q  G  Y  Y  S  T  170

721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T  E  T  M  P  S  R  V  V  C  M  I  E  W  P  E  H  P  N  K  190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I  Y  E  K  V  Y  H  I  C  V  T  V  L  I  Y  F  L  P  L  L  210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V  I  G  Y  A  Y  T  V  V  G  I  T  L  W  A  S  E  I  P  G  230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D  S  S  D  R  Y  H  E  Q  V  S  A  K  R  K  V  V  K  M  M  250
```

FIG. 7B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

FIG. 8A

```
1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60

61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                               M  D  N  V  L  P  V  D  S  D  10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L  S  P  N  I  S  T  N  T  S  E  P  N  Q  F  V  Q  P  A  W  30

301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q  I  V  L  W  A  A  A  Y  T  V  I  V  V  T  S  V  V  G  N  50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V  V  V  M  W  I  I  L  A  H  K  R  M  R  T  V  T  N  Y  F  70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L  V  N  L  A  F  A  E  A  S  M  A  A  F  N  T  V  V  N  F  90

481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T  Y  A  V  H  N  E  W  Y  Y  G  L  F  Y  C  K  F  H  N  F  110

541 TTCCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F  P  I  A  A  V  F  A  S  I  Y  S  M  T  A  V  A  F  D  R  130

601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y  M  A  I  I  H  P  L  Q  P  R  L  S  A  T  A  T  K  V  V  150

661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I  C  V  I  W  V  L  A  L  L  L  A  F  P  Q  G  Y  Y  S  T  170

721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T  E  T  M  P  S  R  V  V  C  M  I  E  W  P  E  H  P  N  K  190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I  Y  E  K  V  Y  H  I  C  V  T  V  L  I  Y  F  L  P  L  L  210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V  I  G  Y  A  Y  T  V  V  G  I  T  L  W  A  S  E  I  P  G  230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D  S  S  D  R  Y  H  E  Q  V  S  A  K  R  K  V  V  K  M  M  250
```

FIG. 8B

```
961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
251 I  V  V  V  C  T  F  A  I  C  W  L  P  F  H  I  F  F  L  L  270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
271 P  Y  I  N  P  D  L  Y  L  K  K  F  I  Q  Q  V  Y  L  A  I  290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
291 M  W  L  A  M  S  S  T  M  Y  N  P  I  I  Y  C  C  L  N  D  310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
311 R  F  R  L  G  F  K  H  A  F  R  C  C  P  F  I  S  A  G  D  330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
331 Y  E  G  L  E  M  K  S  T  R  Y  L  Q  T  Q  G  S  V  Y  K  350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
351 V  S  R  L  E  T  T  I  S  T  V  V  G  A  H  E  E  E  P  E  370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
371 D  G  P  K  A  T  P  S  S  L  D  L  T  S  N  C  S  S  R  S  390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
391 D  S  K  T  M  T  E  S  F  S  F  S  S  N  V  L  S  *        407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766
```

FIG. 9A

```
1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60

61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                                M  D  N  V  L  P  V  D  S  D  10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L  S  P  N  I  S  T  N  T  S  E  P  N  Q  F  V  Q  P  A  W  30

301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q  I  V  L  W  A  A  A  Y  T  V  I  V  V  T  S  V  V  G  N  50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V  V  V  M  W  I  I  L  A  H  K  R  M  R  T  V  T  N  Y  F  70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L  V  N  L  A  F  A  E  A  S  M  A  A  F  N  T  V  V  N  F  90

481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T  Y  A  V  H  N  E  W  Y  Y  G  L  F  Y  C  K  F  H  N  F  110

541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F  P  I  A  A  V  F  A  S  I  Y  S  M  T  A  V  A  F  D  R  130

601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y  M  A  I  I  H  P  L  Q  P  R  L  S  A  T  A  T  K  V  V  150

661 ATCTGTGTCA TATGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I  C  V  I  W  V  L  A  L  L  L  A  F  P  Q  G  Y  Y  S  T  170

721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T  E  T  M  P  S  R  V  V  C  M  I  E  W  P  E  H  P  N  K  190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I  Y  E  K  V  Y  H  I  C  V  T  V  L  I  Y  F  L  P  L  L  210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V  I  G  Y  A  Y  T  V  V  G  I  T  L  W  A  S  E  I  P  G  230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D  S  S  D  R  Y  H  E  Q  V  S  A  K  R  K  V  V  K  M  M  250
```

FIG. 9B

```
961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
251 I  V  V  V   C  T  F   A  I  C   W  L  P  F   H  I  F   F  L  L   270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P  Y  I  N   P  D  L   Y  L  K   K  F  I  Q   Q  V  Y   L  A  I   290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M  W  L  A   M  S  S   T  M  Y   N  P  I  I   Y  C  C   L  N  D   310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R  F  R  L   G  F  K   H  A  F   R  C  C  P   F  I  S   A  G  D   330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y  E  G  L   E  M  K   S  T  R   Y  L  Q  T   Q  G  S   V  Y  K   350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V  S  R  L   E  T  T   I  S  T   V  V  G  A   H  E  E   E  P  E   370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D  G  P  K   A  T  P   S  S  L   D  L  T  S   N  C  S   S  R  S   390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D  S  K  T   M  T  E   S  F  S   F  S  S  N   V  L  S   *           407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766
```

FIG. 10A

```
1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60

61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                               M  D  N  V  L  P  V  D  S  D  10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L  S  P  N  I  S  T  N  T  S  E  P  N  Q  F  V  Q  P  A  W  30

301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q  I  V  L  W  A  A  A  Y  T  V  I  V  V  T  S  V  V  G  N  50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V  V  V  M  W  I  I  L  A  H  K  R  M  R  T  V  T  N  Y  F  70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L  V  N  L  A  F  A  E  A  S  M  A  A  F  N  T  V  V  N  F  90

481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T  Y  A  V  H  N  E  W  Y  Y  G  L  F  Y  C  K  F  H  N  F  110

541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F  P  I  A  A  V  F  A  S  I  Y  S  M  T  A  V  A  F  D  R  130

601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y  M  A  I  I  H  P  L  Q  P  R  L  S  A  T  A  T  K  V  V  150

661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I  C  V  I  W  V  L  A  L  L  L  A  F  P  Q  G  Y  Y  S  T  170

721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T  E  T  M  P  S  R  V  V  C  M  I  E  W  P  E  H  P  N  K  190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I  Y  E  K  V  Y  H  I  C  V  T  V  L  I  Y  F  L  P  L  L  210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V  I  G  Y  A  Y  T  V  V  G  I  T  L  W  A  S  E  I  P  G  230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D  S  S  D  R  Y  H  E  Q  V  S  A  K  R  K  V  V  K  M  M  250
```

FIG. 10B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCATCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

FIG. 11A

```
1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M  A  S  R  L  T  L  L  T  L  L  L  L  L  A  G  D  R  A  20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S  S  N  P  N  A  T  S  S  S  S  Q  D  P  E  S  L  Q  D  R  40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G  E  G  K  V  A  T  T  V  I  S  K  M  L  F  V  E  P  I  L  60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E  V  S  S  L  P  T  T  N  S  T  T  N  S  A  T  K  I  T  A  80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N  T  T  D  E  P  T  T  Q  P  T  T  E  P  T  T  Q  P  T  I  100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q  P  T  Q  P  T  T  Q  L  P  T  D  S  P  T  Q  P  T  T  G  120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S  F  C  P  G  P  V  T  L  C  S  D  L  E  S  H  S  T  E  A  140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V  L  G  D  A  L  V  D  F  S  L  K  L  Y  H  A  F  S  A  M  160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K  K  V  E  T  N  M  A  F  S  P  F  S  I  A  S  L  L  T  Q  180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V  L  L  G  A  G  Q  N  T  K  T  N  L  E  S  I  L  S  Y  P  200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K  D  F  T  C  V  H  Q  A  L  K  G  F  T  T  K  G  V  T  S  220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V  S  Q  I  F  H  S  P  D  L  A  I  R  D  T  F  V  N  A  S  240

781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R  T  L  Y  S  S  S  P  R  V  L  S  N  N  S  D  A  N  L  E  260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L  I  N  T  W  V  A  K  N  T  N  N  K  I  S  R  L  L  D  S  280

901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L  P  S  D  T  R  L  V  L  L  N  A  I  Y  L  S  A  K  W  K  300
```

FIG. 11B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 12A

```
1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M  A  S  R  L  T  L  L  T  L  L  L  L  L  A  G  D  R  A  20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S  S  N  P  N  A  T  S  S  S  S  Q  D  P  E  S  L  Q  D  R  40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G  E  G  K  V  A  T  T  V  I  S  K  M  L  F  V  E  P  I  L  60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E  V  S  S  L  P  T  T  N  S  T  T  N  S  A  T  K  I  T  A  80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N  T  T  D  E  P  T  T  Q  P  T  T  E  P  T  T  Q  P  T  I  100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q  P  T  Q  P  T  T  Q  L  P  T  D  S  P  T  Q  P  T  T  G  120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S  F  C  P  G  P  V  T  L  C  S  D  L  E  S  H  S  T  E  A  140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V  L  G  D  A  L  V  D  F  S  L  K  L  Y  H  A  F  S  A  M  160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K  K  V  E  T  N  M  A  F  S  P  F  S  I  A  S  L  L  T  Q  180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V  L  L  G  A  G  Q  N  T  K  T  N  L  E  S  I  L  S  Y  P  200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K  D  F  T  C  V  H  Q  A  L  K  G  F  T  T  K  G  V  T  S  220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V  S  Q  I  F  H  S  P  D  L  A  I  R  D  T  F  V  N  A  S  240

781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R  T  L  Y  S  S  S  P  R  V  L  S  N  N  S  D  A  N  L  E  260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L  I  N  T  W  V  A  K  N  T  N  N  K  I  S  R  L  L  D  S  280

901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L  P  S  D  T  R  L  V  L  L  N  A  I  Y  L  S  A  K  W  K  300
```

FIG. 12B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGTCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 13A

```
1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M  A  S  R  L  T  L  L  T  L  L  L  L  L  A  G  D  R  A  20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S  S  N  P  N  A  T  S  S  S  S  Q  D  P  E  S  L  Q  D  R  40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGCTGA ACCCATCCTG 240
 41 G  E  G  K  V  A  T  T  V  I  S  K  M  L  F  A  E  P  I  L  60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E  V  S  S  L  P  T  T  N  S  T  T  N  S  A  T  K  I  T  A  80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N  T  T  D  E  P  T  T  Q  P  T  T  E  P  T  T  Q  P  T  I  100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q  P  T  Q  P  T  T  Q  L  P  T  D  S  P  T  Q  P  T  T  G  120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S  F  C  P  G  P  V  T  L  C  S  D  L  E  S  H  S  T  E  A  140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V  L  G  D  A  L  V  D  F  S  L  K  L  Y  H  A  F  S  A  M  160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K  K  V  E  T  N  M  A  F  S  P  F  S  I  A  S  L  L  T  Q  180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V  L  L  G  A  G  Q  N  T  K  T  N  L  E  S  I  L  S  Y  P  200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K  D  F  T  C  V  H  Q  A  L  K  G  F  T  T  K  G  V  T  S  220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V  S  Q  I  F  H  S  P  D  L  A  I  R  D  T  F  V  N  A  S  240

781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R  T  L  Y  S  S  S  P  R  V  L  S  N  N  S  D  A  N  L  E  260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L  I  N  T  W  V  A  K  N  T  N  N  K  I  S  R  L  L  D  S  280

901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L  P  S  D  T  R  L  V  L  L  N  A  I  Y  L  S  A  K  W  K  300
```

FIG. 13B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 14A

```
 1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M  A  S  R  L  T  L  L  T  L  L  L  L  L  A  G  D  R  A  20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S  S  N  P  N  A  T  S  S  S  S  Q  D  P  E  S  L  Q  D  R  40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G  E  G  K  V  A  T  T  V  I  S  K  M  L  F  V  E  P  I  L  60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E  V  S  S  L  P  T  T  N  S  T  T  N  S  A  T  K  I  T  A  80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N  T  T  D  E  P  T  T  Q  P  T  T  E  P  T  T  Q  P  T  I  100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q  P  T  Q  P  T  T  Q  L  P  T  D  S  P  T  Q  P  T  T  G  120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S  F  C  P  G  P  V  T  L  C  S  D  L  E  S  H  S  T  E  A  140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGGAATG 540
141 V  L  G  D  A  L  V  D  F  S  L  K  L  Y  H  A  F  S  G  M  160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K  K  V  E  T  N  M  A  F  S  P  F  S  I  A  S  L  L  T  Q  180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V  L  L  G  A  G  Q  N  T  K  T  N  L  E  S  I  L  S  Y  P  200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K  D  F  T  C  V  H  Q  A  L  K  G  F  T  T  K  G  V  T  S  220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V  S  Q  I  F  H  S  P  D  L  A  I  R  D  T  F  V  N  A  S  240

781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R  T  L  Y  S  S  S  P  R  V  L  S  N  N  S  D  A  N  L  E  260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L  I  N  T  W  V  A  K  N  T  N  N  K  I  S  R  L  L  D  S  280

901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L  P  S  D  T  R  L  V  L  L  N  A  I  Y  L  S  A  K  W  K  300
```

FIG. 14B

```
961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
301 T  T  F  D   P  K  K   T  R  M   E  P  F  H   F  K  N   S  V  I   320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
321 K  V  P  M   M  N  S   K  K  Y   P  V  A  H   F  I  D   Q  T  L   340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
341 K  A  K  V   G  Q  L   Q  L  S   H  N  L  S   L  V  I   L  V  P   360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
361 Q  N  L  K   H  R  L   E  D  M   E  Q  A  L   S  P  S   V  F  K   380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
381 A  I  M  E   K  L  E   M  S  K   F  Q  P  T   L  L  T   L  P  R   400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
401 I  K  V  T   T  S  Q   D  M  L   S  I  M  E   K  L  E   F  F  D   420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
421 F  S  Y  D   L  N  L   C  G  L   T  E  D  P   D  L  Q   V  S  A   440

1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
441 M  Q  H  Q   T  V  L   E  L  T   E  T  G  V   E  A  A   A  A  S   460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
461 A  I  S  V   A  R  T   L  L  V   F  E  V  Q   Q  P  F   L  F  V   480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
481 L  W  D  Q   Q  H  K   F  P  V   F  M  G  R   V  Y  D   P  R  A   500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826
```

FIG. 15A

```
1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M  A  S  R  L  T  L  L  T  L  L  L  L  L  A  G  D  R  A  20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S  S  N  P  N  A  T  S  S  S  S  Q  D  P  E  S  L  Q  D  R  40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G  E  G  K  V  A  T  T  V  I  S  K  M  L  F  V  E  P  I  L  60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E  V  S  S  L  P  T  T  N  S  T  T  N  S  A  T  K  I  T  A  80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N  T  T  D  E  P  T  T  Q  P  T  T  E  P  T  T  Q  P  T  I  100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q  P  T  Q  P  T  T  Q  L  P  T  D  S  P  T  Q  P  T  T  G  120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S  F  C  P  G  P  V  T  L  C  S  D  L  E  S  H  S  T  E  A  140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V  L  G  D  A  L  V  D  F  S  L  K  L  Y  H  A  F  S  A  M  160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K  K  V  E  T  N  M  A  F  S  P  F  S  I  A  S  L  L  T  Q  180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V  L  L  G  A  G  Q  N  T  K  T  N  L  E  S  I  L  S  Y  P  200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K  D  F  T  C  V  H  Q  A  L  K  G  F  T  T  K  G  V  T  S  220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V  S  Q  I  F  H  S  P  D  L  A  I  R  D  T  F  V  N  A  S  240

781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R  T  L  Y  S  S  S  P  R  V  L  S  N  N  S  D  A  N  L  E  260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L  I  N  T  W  V  A  K  N  T  N  N  K  I  S  R  L  L  D  S  280

901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L  P  S  D  T  R  L  V  L  L  N  A  I  Y  L  S  A  K  W  K  300
```

FIG. 15B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCATG 1500
461 A I S V A R T L L V F E V Q Q P F L F M 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 16

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1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
1                                   M  W  F  L  V  L  C  L   8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A  L  S  L  G  G  T  G  A  A  P  P  I  Q  S  R  I  V  G  G  28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
 29 W  E  C  E  Q  H  S  Q  P  W  Q  A  A  L  Y  H  F  S  T  F  48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q  C  G  G  I  L  V  H  R  Q  W  V  L  T  A  A  H  C  I  S  68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D  N  Y  Q  L  W  L  G  R  H  N  L  F  D  D  E  N  T  A  Q  88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F  V  H  V  S  E  S  F  P  H  P  G  F  N  M  S  L  L  E  N  108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H  T  R  Q  A  D  E  D  Y  S  H  D  L  M  L  L  R  L  T  E  128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCGA GGAACCCGAA 480
129 P  A  D  T  I  T  D  A  V  K  V  V  E  L  P  T  E  E  P  E  148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V  G  S  T  C  L  A  S  G  W  G  S  I  E  P  E  N  F  S  F  168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAAGCC 600
169 P  D  D  L  Q  C  V  D  L  K  I  L  P  N  D  E  C  K  K  A  188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H  V  Q  K  V  T  D  F  M  L  C  V  G  H  L  E  G  G  K  D  208

661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T  C  V  G  D  S  G  G  P  L  M  C  D  G  V  L  Q  G  V  T  228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S  W  G  Y  V  P  C  G  T  P  N  K  P  S  V  A  V  R  V  L  248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S  Y  V  K  W  I  E  D  T  I  A  E  N  S  *                   262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871
```

FIG. 17

```
1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
1                                          M  W  F  L  V  L  C  L   8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A  L  S  L  G  G  T  G  A  A  P  P  I  Q  S  R  I  V  G  G   28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
 29 W  E  C  E  Q  H  S  Q  P  W  Q  A  A  L  Y  H  F  S  T  F   48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q  C  G  G  I  L  V  H  R  Q  W  V  L  T  A  A  H  C  I  S   68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D  N  Y  Q  L  W  L  G  R  H  N  L  F  D  D  E  N  T  A  Q   88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F  V  H  V  S  E  S  F  P  H  P  G  F  N  M  S  L  L  E  N  108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H  T  R  Q  A  D  E  D  Y  S  H  D  L  M  L  L  R  L  T  E  128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCGA GGAACCCGAA 480
129 P  A  D  T  I  T  D  A  V  K  V  V  E  L  P  T  E  E  P  E  148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V  G  S  T  C  L  A  S  G  W  G  S  I  E  P  E  N  F  S  F  168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CGAAAAAGCC 600
169 P  D  D  L  Q  C  V  D  L  K  I  L  P  N  D  E  C  E  K  A  188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H  V  Q  K  V  T  D  F  M  L  C  V  G  H  L  E  G  G  K  D  208

661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T  C  V  G  D  S  G  G  P  L  M  C  D  G  V  L  Q  G  V  T  228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S  W  G  Y  V  P  C  G  T  P  N  K  P  S  V  A  V  R  V  L  248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S  Y  V  K  W  I  E  D  T  I  A  E  N  S  *                   262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871
```

FIG. 18

```
1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
1                                   M  W  F  L  V  L  C  L   8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A  L  S  L  G  G  T  G  A  A  P  P  I  Q  S  R  I  V  G  G  28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
 29 W  E  C  E  Q  H  S  Q  P  W  Q  A  A  L  Y  H  F  S  T  F  48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q  C  G  G  I  L  V  H  R  Q  W  V  L  T  A  A  H  C  I  S  68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D  N  Y  Q  L  W  L  G  R  H  N  L  F  D  D  E  N  T  A  Q  88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F  V  H  V  S  E  S  F  P  H  P  G  F  N  M  S  L  L  E  N  108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H  T  R  Q  A  D  E  D  Y  S  H  D  L  M  L  L  R  L  T  E  128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCCA GGAACCCGAA 480
129 P  A  D  T  I  T  D  A  V  K  V  V  E  L  P  T  Q  E  P  E  148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V  G  S  T  C  L  A  S  G  W  G  S  I  E  P  E  N  F  S  F  168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAAGCC 600
169 P  D  D  L  Q  C  V  D  L  K  I  L  P  N  D  E  C  K  K  A  188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H  V  Q  K  V  T  D  F  M  L  C  V  G  H  L  E  G  G  K  D  208

661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T  C  V  G  D  S  G  G  P  L  M  C  D  G  V  L  Q  G  V  T  228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S  W  G  Y  V  P  C  G  T  P  N  K  P  S  V  A  V  R  V  L  248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S  Y  V  K  W  I  E  D  T  I  A  E  N  S  *                   262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871
```

FIG. 19

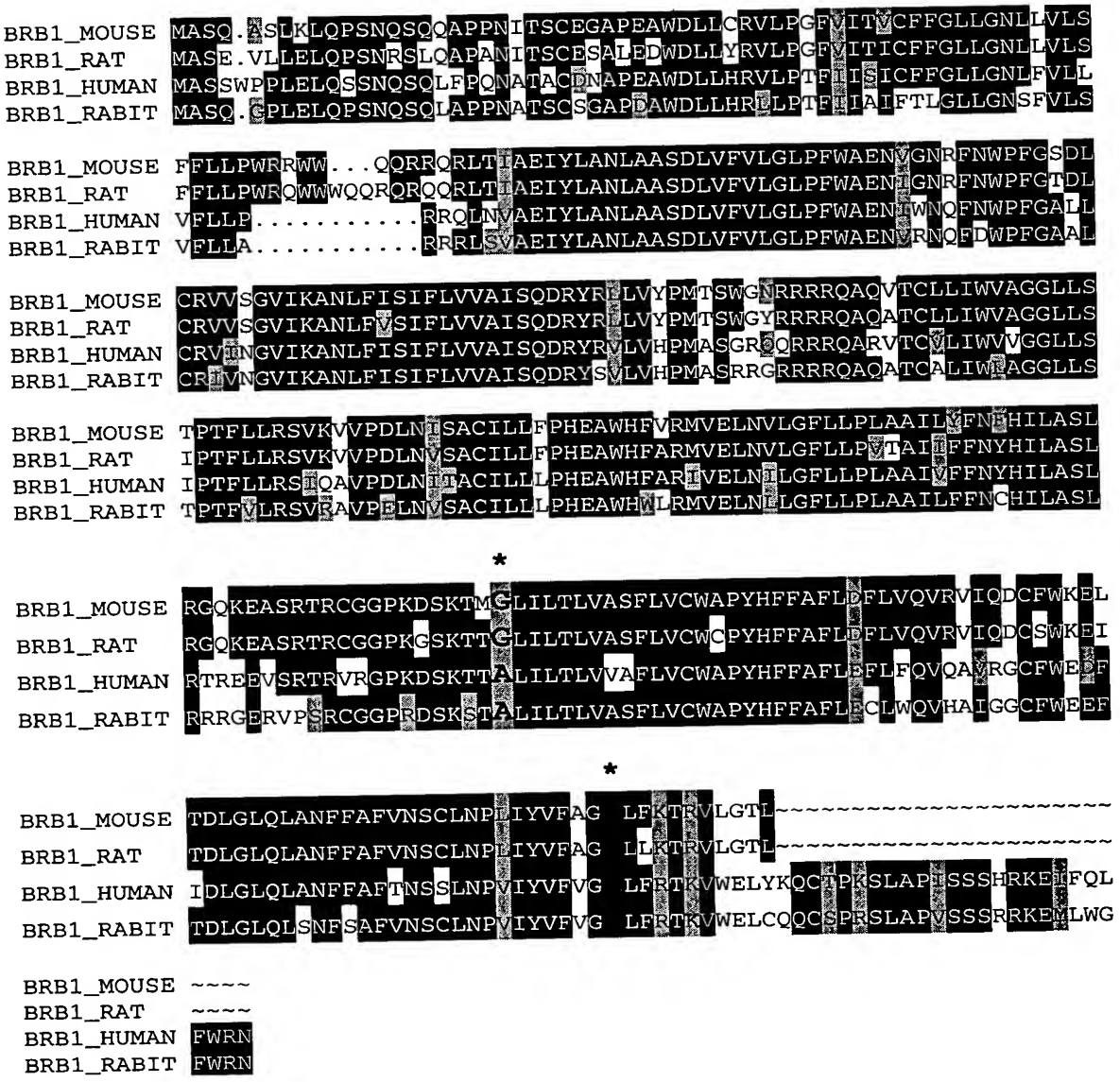

FIG. 20

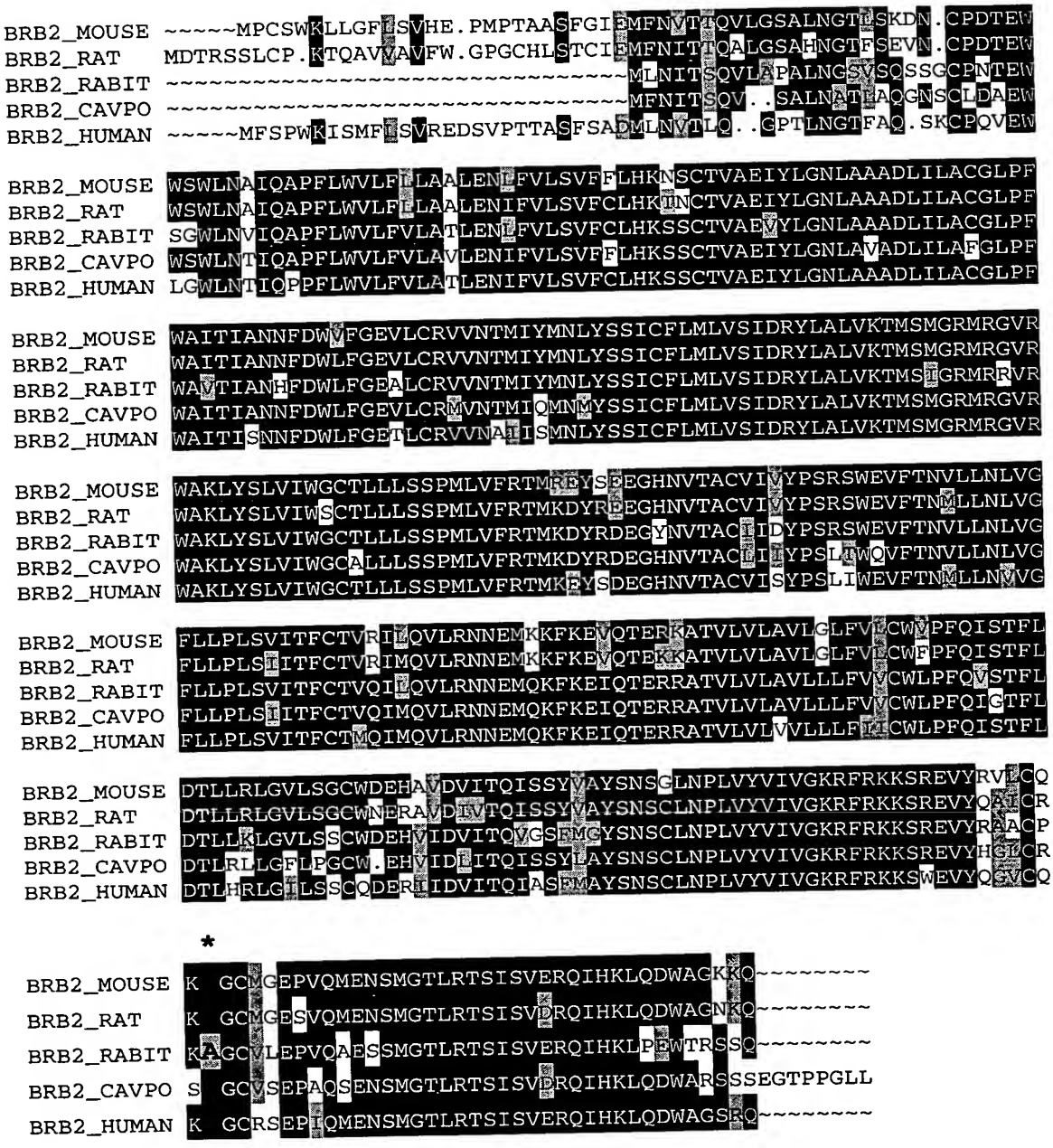

FIG. 21A

```
 1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1       M  A  S  S  W  P  P  L  E  L  Q  S  S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCNA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAANGG GGTCATCAAG 360
99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GNCAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCNTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  X  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGANGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  E  E  V  S  R  T  238

721 AGAGTGCNGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  X  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 21B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCNGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  X  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 22A

```
   1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC  60

  61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120

 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
   1                               M  D  N  V  L  P  V  D  S  D   10

 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
  11 L  S  P  N  I  S  T  N  T  S  E  P  N  Q  F  V  Q  P  A  W   30

 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
  31 Q  I  V  L  W  A  A  A  Y  T  V  I  V  V  T  S  V  V  G  N   50

 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
  51 V  V  V  M  W  I  I  L  A  H  K  R  M  R  T  V  T  N  Y  F   70

 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
  71 L  V  N  L  A  F  A  E  A  S  M  A  A  F  N  T  V  V  N  F   90

 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
  91 T  Y  A  V  H  N  E  W  Y  Y  G  L  F  Y  C  K  F  H  N  F  110

 541 TTNCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F  P  I  A  A  V  F  A  S  I  Y  S  M  T  A  V  A  F  D  R  130

 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y  M  A  I  I  H  P  L  Q  P  R  L  S  A  T  A  T  K  V  V  150

 661 ATCTGTGTCA TNTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I  C  V  I  W  V  L  A  L  L  L  A  F  P  Q  G  Y  Y  S  T  170

 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T  E  T  M  P  S  R  V  V  C  M  I  E  W  P  E  H  P  N  K  190

 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I  Y  E  K  V  Y  H  I  C  V  T  V  L  I  Y  F  L  P  L  L  210

 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V  I  G  Y  A  Y  T  V  V  G  I  T  L  W  A  S  E  I  P  G  230

 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D  S  S  D  R  Y  H  E  Q  V  S  A  K  R  K  V  V  K  M  M  250
```

FIG. 22B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCNTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

FIG. 23A

```
1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M  A  S  R  L  T  L  L  T  L  L  L  L  L  A  G  D  R  A  20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S  S  N  P  N  A  T  S  S  S  S  Q  D  P  E  S  L  Q  D  R  40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGNTGA ACCCATCCTG 240
 41 G  E  G  K  V  A  T  T  V  I  S  K  M  L  F  X  E  P  I  L  60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E  V  S  S  L  P  T  T  N  S  T  T  N  S  A  T  K  I  T  A  80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N  T  T  D  E  P  T  T  Q  P  T  T  E  P  T  T  Q  P  T  I  100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q  P  T  Q  P  T  T  Q  L  P  T  D  S  P  T  Q  P  T  T  G  120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S  F  C  P  G  P  V  T  L  C  S  D  L  E  S  H  S  T  E  A  140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGNAATG 540
141 V  L  G  D  A  L  V  D  F  S  L  K  L  Y  H  A  F  S  X  M  160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K  K  V  E  T  N  M  A  F  S  P  F  S  I  A  S  L  L  T  Q  180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V  L  L  G  A  G  Q  N  T  K  T  N  L  E  S  I  L  S  Y  P  200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K  D  F  T  C  V  H  Q  A  L  K  G  F  T  T  K  G  V  T  S  220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V  S  Q  I  F  H  S  P  D  L  A  I  R  D  T  F  V  N  A  S  240

781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R  T  L  Y  S  S  S  P  R  V  L  S  N  N  S  D  A  N  L  E  260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L  I  N  T  W  V  A  K  N  T  N  N  K  I  S  R  L  L  D  S  280

901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L  P  S  D  T  R  L  V  L  L  N  A  I  Y  L  S  A  K  W  K  300
```

FIG. 23B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGNCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCNTG 1500
461 A I S V A R T L L V F E V Q Q P F L F X 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 24

```
1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
1                                   M  W  F  L  V  L  C  L   8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A  L  S  L  G  G  T  G  A  A  P  P  I  Q  S  R  I  V  G  G  28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
 29 W  E  C  E  Q  H  S  Q  P  W  Q  A  A  L  Y  H  F  S  T  F  48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q  C  G  G  I  L  V  H  R  Q  W  V  L  T  A  A  H  C  I  S  68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D  N  Y  Q  L  W  L  G  R  H  N  L  F  D  D  E  N  T  A  Q  88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F  V  H  V  S  E  S  F  P  H  P  G  F  N  M  S  L  L  E  N  108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H  T  R  Q  A  D  E  D  Y  S  H  D  L  M  L  L  R  L  T  E  128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCNA GGAACCCGAA 480
129 P  A  D  T  I  T  D  A  V  K  V  V  E  L  P  T  X  E  P  E  148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V  G  S  T  C  L  A  S  G  W  G  S  I  E  P  E  N  F  S  F  168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CNAAAAAGCC 600
169 P  D  D  L  Q  C  V  D  L  K  I  L  P  N  D  E  C  X  K  A  188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H  V  Q  K  V  T  D  F  M  L  C  V  G  H  L  E  G  G  K  D  208

661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T  C  V  G  D  S  G  G  P  L  M  C  D  G  V  L  Q  G  V  T  228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S  W  G  Y  V  P  C  G  T  P  N  K  P  S  V  A  V  R  V  L  248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S  Y  V  K  W  I  E  D  T  I  A  E  N  S  *                    262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871
```

FIG. 25A

```
1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1       M  A  S  S  W  P  P  L  E  L  Q  S   S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAATGG GGTCATCAAG 360
99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  L  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  E  E  V  S  R  T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  R  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 25B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  R  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 26A

```
1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1       M  A  S  S  W  P  P  L  E  L  Q  S  S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GACAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  L  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  E  E  V  S  R  T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  R  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 26B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  R  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 27A

```
1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1       M  A  S  S  W  P  P  L  E  L  Q  S  S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCGTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  V  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  E  E  V  S  R  T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  R  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 27B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  R  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 28A

```
1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1       M  A  S  S  W  P  P  L  E  L  Q  S  S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  L  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  K  E  V  S  R  T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  R  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 28B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  R  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 29A

```
1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC 60
1 M  F  S  P  W  K  I  S  M  F  L  S  V  C  E  D  S  V  P  T  20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G  40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q  60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S  80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  V  L  L  L  F  I  280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

FIG. 29B

```
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
301 L  S  S  C   Q  D  E   R  I  I   D  V  I  T   Q  I  A   S  F  M   320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
321 A  Y  S  N   S  C  L   N  P  L   V  Y  V  I   V  G  K   R  F  R   340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
341 K  K  S  W   E  V  Y   Q  G  V   C  Q  K  G   G  C  R   S  E  P   360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
361 I  Q  M  E   N  S  M   G  T  L   R  T  S  I   S  V  E   R  Q  I   380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
381 H  K  L  Q   D  W  A   G  S  R   Q  *                              391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

FIG. 29C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 29D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733

FIG. 30A

```
  1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC 60
  1 M  F  S  P  W  K  I  S  M  F  L  S  V  R  E  D  S  V  P  T  20

 61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
 21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G  40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q  60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
 61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S  80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  V  L  L  L  F  I  280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

FIG. 30B

```
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GACGTAATCA CACAGATCGC CTCCTTCATG 960
301 L  S  S  C   Q  D  E   R  I  I   D  V  I  T   Q  I  A   S  F  M   320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
321 A  Y  S  N   S  C  L   N  P  L   V  Y  V  I   V  G  K   R  F  R   340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
341 K  K  S  W   E  V  Y   Q  G  V   C  Q  K  G   G  C  R   S  E  P   360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
361 I  Q  M  E   N  S  M   G  T  L   R  T  S  I   S  V  E   R  Q  I   380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
381 H  K  L  Q   D  W  A   G  S  R   Q  *                              391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

FIG. 30C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 30D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733

FIG. 31A

```
 1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC 60
 1 M  F  S  P  W  K  I  S  M  F  L  S  V  R  E  D  S  V  P  T  20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G  40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q  60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S  80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  V  L  L  L  F  I  280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

FIG. 31B

```
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
301 L  S  S  C   Q  D  E   R  I  I   D  V  I  T   Q  I  A   S  F  M   320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
321 A  Y  S  N   S  C  L   N  P  L   V  Y  V  I   V  G  K   R  F  R   340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG AGGGCTGCAG GTCAGAACCC 1080
341 K  K  S  W   E  V  Y   Q  G  V   C  Q  K  E   G  C  R   S  E  P   360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
361 I  Q  M  E   N  S  M   G  T  L   R  T  S  I   S  V  E   R  Q  I   380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
381 H  K  L  Q   D  W  A   G  S  R   Q  *                              391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

FIG. 31C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 31D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733

FIG. 32A

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   1  CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTTAGTCTA   60

  61  GGGAAAGTCATTCAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTG  120
   1                                                  M  S  S  S  S  W    6

 121  GCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACCATTGAGGAACAGGCCAA  180
   7   L  L  L  S  L  V  A  V  T  A  A  Q  S  T  I  E  E  Q  A  K   26

 181  GACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC  240
  27   T  F  L  D  K  F  N  H  E  A  E  D  L  F  Y  Q  S  S  L  A   46

 241  TTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG  300
  47   S  W  N  Y  N  T  N  I  T  E  E  N  V  Q  N  M  N  N  A  G   66

 301  GGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA  360
  67   D  K  W  S  A  F  L  K  E  Q  S  T  L  A  Q  M  Y  P  L  Q   86

 361  AGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC  420
  87   E  I  Q  N  L  T  V  K  L  Q  L  Q  A  L  Q  Q  N  G  S  S  106

 421  AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT  480
 107   V  L  S  E  D  K  S  K  R  L  N  T  I  L  N  T  M  S  T  I  126

 481  CTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC  540
 127   Y  S  T  G  K  V  C  N  P  D  N  P  Q  E  C  L  L  L  E  P  146

 541  AGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA  600
 147   G  L  N  E  I  M  A  N  S  L  D  Y  N  E  R  L  W  A  W  E  166

 601  AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT  660
 167   S  W  R  S  E  V  G  K  Q  L  R  P  L  Y  E  E  Y  V  V  L  186

 661  GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA  720
 187   K  N  E  M  A  R  A  N  H  Y  E  D  Y  G  D  Y  W  R  G  D  206

 721  CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGT  780
 207   Y  E  V  N  G  V  D  G  Y  D  Y  S  R  G  Q  L  I  E  D  V  226

 781  GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC  840
 227   E  H  T  F  E  E  I  K  P  L  Y  E  H  L  H  A  Y  V  R  A  246

 841  AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT  900
 247   K  L  M  N  A  Y  P  S  Y  I  S  P  I  G  C  L  P  A  H  L  266
```

FIG. 32B

```
901  GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCCTTTGG  960
267    L  G  D  M  W  G  R  F  W  T  N  L  Y  S  L  T  V  P  F  G  286

961  ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG  1020
287    Q  K  P  N  I  D  V  T  D  A  M  V  D  Q  A  W  D  A  Q  R  306

1021 AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGG  1080
307    I  F  K  E  A  E  K  F  F  V  S  V  G  L  P  N  M  T  Q  G  326

1081 ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAGAAAGCAGTCTGCCATCC  1140
327    F  W  E  N  S  M  L  T  D  P  G  N  V  Q  K  A  V  C  H  P  346

1141 CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT  1200
347    T  A  W  D  L  G  K  G  D  F  R  I  L  M  C  T  K  V  T  M  366

1201 GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC  1260
367    D  D  F  L  T  A  H  H  E  M  G  H  I  Q  Y  D  M  A  Y  A  386

1261 TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGA  1320
387    A  Q  P  F  L  L  R  N  G  A  N  E  G  F  H  E  A  V  G  E  406

1321 AATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCACC  1380
407    I  M  S  L  S  A  A  T  P  K  H  L  K  S  I  G  L  L  S  P  426

1381 CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT  1440
427    D  F  Q  E  D  N  E  T  E  I  N  F  L  L  K  Q  A  L  T  I  446

1441 TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG  1500
447    V  G  T  L  P  F  T  Y  M  L  E  K  W  R  W  M  V  F  K  G  466

1501 GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG  1560
467    E  I  P  K  D  Q  W  M  K  K  W  W  E  M  K  R  E  I  V  G  486

1561 GGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGT  1620
487    V  V  E  P  V  P  H  D  E  T  Y  C  D  P  A  S  L  F  H  V  506

1621 TTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTTTACCAATTCCAGTTTCA  1680
507    S  N  D  Y  S  F  I  R  Y  Y  T  R  T  L  Y  Q  F  Q  F  Q  526

1681 AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA  1740
527    E  A  L  C  Q  A  A  K  H  E  G  P  L  H  K  C  D  I  S  N  546
```

FIG. 32C

```
1741  CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCTG  1800
 547    S  T  E  A  G  Q  K  L  F  N  M  L  R  L  G  K  S  E  P  W    566

1801  GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA  1860
 567    T  L  A  L  E  N  V  V  G  A  K  N  M  N  V  R  P  L  L  N    586

1861  CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATG  1920
 587    Y  F  E  P  L  F  T  W  L  K  D  Q  N  K  N  S  F  V  G  W    606

1921  GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC  1980
 607    S  T  D  W  S  P  Y  A  D  Q  S  I  K  V  R  I  S  L  K  S    626

1981  AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC  2040
 627    A  L  G  D  K  A  Y  E  W  N  D  N  E  M  Y  L  F  R  S  S    646

2041  TGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGG  2100
 647    V  A  Y  A  M  R  Q  Y  F  L  K  V  K  N  Q  M  I  L  F  G    666

2101  GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCAC  2160
 667    E  E  D  V  R  V  A  N  L  K  P  R  I  S  F  N  F  F  V  T    686

2161  TGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGAT  2220
 687    A  P  K  N  V  S  D  I  I  P  R  T  E  V  E  K  A  I  R  M    706

2221  GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG  2280
 707    S  R  S  R  I  N  D  A  F  R  L  N  D  N  S  L  E  F  L  G    726

2281  GATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTT  2340
 727    I  Q  P  T  L  G  P  P  N  Q  P  P  V  S  I  W  L  I  V  F    746

2341  TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG  2400
 747    G  V  V  M  G  V  I  V  V  G  I  V  I  L  I  F  T  G  I  R    766

2401  AGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT  2460
 767    D  R  K  K  K  N  K  A  R  S  G  E  N  P  Y  A  S  I  D  I    786

2461  TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTTTTA  2520
 787    S  K  G  E  N  N  P  G  F  Q  N  T  D  D  V  Q  T  S  F  *    806

2521  GAAAAATCTATGTTTTTCCTCTTGAGGTGATTTTGTTGTATGTAAATGTTAATTTCATGG  2580

2581  TATAGAAAATATAAGATGATAAAGATATCATTAAATGTCAAAACTATGACTCTGTTCAGA  2640
```

FIG. 32D

```
2641  AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC  2700

2701  AGTATTTATTTCTGTCTCTGGATTTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGTAT  2760

2761  TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTCAGGGATAATCTAAAT  2820

2821  GTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTTG  2880

2881  GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAACTGGTGTAGC  2940

2941  TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA  3000

3001  CATGCTTTCTTCACAGTAACTCAGTTCAAGTACTATGGTGATTTGCCTACAGTGATGTTT  3060

3061  GGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG  3120

3121  GTAGAGGACATTGCTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA  3180

3181  AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAAACTCATTTCTAC  3240

3241  TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACTGTATGTTCACCCTCTGAAGTGGGT  3300

3301  ACCCAGTCTCTTAAATCTTTTGTATTTGCTCACAGTGTTTGAGCAGTGCTGAGCACAAAG  3360

3361  CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAA  3405
```

FIG. 33A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1  M  H  L  I  D  Y  L  L  L  L  L  V  G  L  L  A  L  S  H  G    20

 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21  Q  L  H  V  E  H  D  G  E  S  C  S  N  S  S  H  Q  Q  I  L    40

121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41  E  T  G  E  G  S  P  S  L  K  I  A  P  A  N  A  D  F  A  F    60

181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61  R  F  Y  Y  L  I  A  S  E  T  P  G  K  N  I  F  F  S  P  L    80

241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81  S  I  S  A  A  Y  A  M  L  S  L  G  A  C  S  H  S  R  S  Q   100

301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101  I  L  E  G  L  G  F  N  L  T  E  L  S  E  S  D  V  H  R  G   120

361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC  420
121  F  Q  H  L  L  H  T  L  N  L  P  G  H  G  L  E  T  R  V  G   140

421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141  S  A  L  F  L  S  H  N  L  K  F  L  A  K  F  L  N  D  T  M   160

481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161  A  V  Y  E  A  K  L  F  H  T  N  F  Y  D  T  V  G  T  I  Q   180

541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG  600
181  L  I  N  D  H  V  K  K  E  T  R  G  K  I  V  D  L  V  S  E   200

601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201  L  K  K  D  V  L  M  V  L  V  N  Y  I  Y  F  K  A  L  W  E   220

661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA  720
221  K  P  F  I  S  S  R  T  T  P  K  D  F  Y  V  D  E  N  T  T   240

721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241  V  R  V  P  M  M  L  Q  D  Q  E  H  H  W  Y  L  H  D  R  Y   260

781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261  L  P  C  S  V  L  R  M  D  Y  K  G  D  A  T  V  F  F  I  L   280
```

FIG. 33B

```
841   CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
281   P  N  Q  G  K  M  R  E  I  E  E  V  L  T  P  E  M  L  M  R    300

901   TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
301   W  N  N  L  L  R  K  R  N  F  Y  K  K  L  E  L  H  L  P  K    320

961   TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT   1020
321   F  S  I  S  G  S  Y  V  L  D  Q  I  L  P  R  L  G  F  T  D    340

1021  CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC   1080
341   L  F  S  K  W  A  D  L  S  G  I  T  K  Q  Q  K  L  E  A  S    360

1081  AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   1140
361   K  S  F  H  K  A  T  L  D  V  D  E  A  G  T  E  A  A  A  A    380

1141  ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC   1200
381   T  T  F  A  I  K  F  F  S  A  Q  T  N  R  H  I  L  R  F  N    400

1201  CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG   1260
401   R  P  F  L  V  V  I  F  S  T  S  T  Q  S  V  L  F  L  G  K    420

1261  GTCGTCGACCCCACGAAACCATAG  1284
421   V  V  D  P  T  K  P  *   428
```

FIG. 34A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1  M  H  L  I  D  Y  L  L  L  L  L  V  G  L  L  A  L  S  H  G    20

 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21  Q  L  H  V  E  H  D  G  E  S  C  S  N  S  S  H  Q  Q  I  L    40

121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41  E  T  G  E  G  S  P  S  L  K  I  A  P  A  N  A  D  F  A  F    60

181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61  R  F  Y  Y  L  I  A  S  E  T  P  G  K  N  I  F  F  S  P  L    80

241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81  S  I  S  A  A  Y  A  M  L  S  L  G  A  C  S  H  S  R  S  Q   100

301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101  I  L  E  G  L  G  F  N  L  T  E  L  S  E  S  D  V  H  R  G   120

361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC  420
121  F  Q  H  L  L  H  T  L  N  L  P  G  H  G  L  E  T  R  V  G   140

421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141  S  A  L  F  L  S  H  N  L  K  F  L  A  K  F  L  N  D  T  M   160

481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161  A  V  Y  E  A  K  L  F  H  T  N  F  Y  D  T  V  G  T  I  Q   180

541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG  600
181  L  I  N  D  H  V  K  K  E  T  R  G  K  I  V  D  L  V  S  E   200

601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201  L  K  K  D  V  L  M  V  L  V  N  Y  I  Y  F  K  A  L  W  E   220

661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTTTATGTTGATGAGAACACAACA  720
221  K  P  F  I  S  S  R  T  T  P  K  D  F  Y  V  D  E  N  T  T   240

721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241  V  R  V  P  M  M  L  Q  D  Q  E  H  H  W  Y  L  H  D  R  Y   260

781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261  L  P  C  S  V  L  R  M  D  Y  K  G  D  A  T  V  F  F  I  L   280
```

FIG. 34B

```
841  CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
281  P  N  Q  G  K  M  R  E  I  E  E  V  L  T  P  E  M  L  M  R    300

901  TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
301  W  N  N  L  L  R  K  R  N  F  Y  K  K  L  E  L  H  L  P  K    320

961  TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT   1020
321  F  S  I  S  G  S  Y  V  L  D  Q  I  L  P  R  L  G  F  T  D    340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC   1080
341  L  F  S  K  W  A  D  L  S  G  I  T  K  Q  Q  K  L  E  A  S    360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   1140
361  K  S  F  H  K  A  T  L  D  V  D  E  A  G  T  E  A  A  A  A    380

1141 ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC   1200
381  T  T  F  A  I  K  F  F  S  A  Q  T  N  R  H  I  L  R  F  N    400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG   1260
401  R  P  F  L  V  V  I  F  S  T  S  T  Q  S  V  L  F  L  G  K    420

1261 GTCGTCGACCCCACGAAACCATAG  1284
421  V  V  D  P  T  K  P  *    428
```

FIG. 35A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1  M  H  L  I  D  Y  L  L  L  L  L  V  G  L  L  A  L  S  H  G    20

 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21  Q  L  H  V  E  H  D  G  E  S  C  S  N  S  S  H  Q  Q  I  L    40

121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41  E  T  G  E  G  S  P  S  L  K  I  A  P  A  N  A  D  F  A  F    60

181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61  R  F  Y  Y  L  I  A  S  E  T  P  G  K  N  I  F  F  S  P  L    80

241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81  S  I  S  A  A  Y  A  M  L  S  L  G  A  C  S  H  S  R  S  Q   100

301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101  I  L  E  G  L  G  F  N  L  T  E  L  S  E  S  D  V  H  R  G   120

361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC  420
121  F  Q  H  L  L  H  T  L  N  L  P  G  H  G  L  E  T  R  V  G   140

421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141  S  A  L  F  L  S  H  N  L  K  F  L  A  K  F  L  N  D  T  M   160

481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161  A  V  Y  E  A  K  L  F  H  T  N  F  Y  D  T  V  G  T  I  Q   180

541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGCGAG  600
181  L  I  N  D  H  V  K  K  E  T  R  G  K  I  V  D  L  V  S  E   200

601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201  L  K  K  D  V  L  M  V  L  V  N  Y  I  Y  F  K  A  L  W  E   220

661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA  720
221  K  P  F  I  S  S  R  T  T  P  K  D  F  Y  V  D  E  N  T  T   240

721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241  V  R  V  P  M  M  L  Q  D  Q  E  H  H  W  Y  L  H  D  R  Y   260

781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261  L  P  C  S  V  L  R  M  D  Y  K  G  D  A  T  V  F  F  I  L   280
```

FIG. 35B

```
 841  CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
 281  P  N  Q  G  K  M  R  E  I  E  E  V  L  T  P  E  M  L  M  R    300

 901  TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
 301  W  N  N  L  L  R  K  R  N  F  Y  K  K  L  E  L  H  L  P  K    320

 961  TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT   1020
 321  F  S  I  S  G  S  Y  V  L  D  Q  I  L  P  R  L  G  F  T  D    340

1021  CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC   1080
 341  L  F  S  K  W  A  D  L  S  G  I  T  K  Q  Q  K  L  E  A  S    360

1081  AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   1140
 361  K  S  F  H  K  A  T  L  D  V  D  E  A  G  T  E  A  A  A  A    380

1141  ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC   1200
 381  T  T  F  A  I  K  F  F  S  A  Q  T  N  R  H  I  L  R  F  N    400

1201  CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG   1260
 401  R  P  F  L  V  V  I  F  S  T  S  T  Q  S  V  L  F  L  G  K    420

1261  GTCGTCGACCCCACGAAACCATAG  1284
 421  V  V  D  P  T  K  P  *   428
```

FIG. 36A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1  M  H  L  I  D  Y  L  L  L  L  L  V  G  L  L  A  L  S  H  G    20

 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21  Q  L  H  V  E  H  D  G  E  S  C  S  N  S  S  H  Q  Q  I  L    40

121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41  E  T  G  E  G  S  P  S  L  K  I  A  P  A  N  A  D  F  A  F    60

181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61  R  F  Y  Y  L  I  A  S  E  T  P  G  K  N  I  F  F  S  P  L    80

241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81  S  I  S  A  A  Y  A  M  L  S  L  G  A  C  S  H  S  R  S  Q   100

301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101  I  L  E  G  L  G  F  N  L  T  E  L  S  E  S  D  V  H  R  G   120

361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC  420
121  F  Q  H  L  L  H  T  L  N  L  P  G  H  G  L  E  T  R  V  G   140

421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141  S  A  L  F  L  S  H  N  L  K  F  L  A  K  F  L  N  D  T  M   160

481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161  A  V  Y  E  A  K  L  F  H  T  N  F  Y  D  T  V  G  T  I  Q   180

541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGNGAG  600
181  L  I  N  D  H  V  K  K  E  T  R  G  K  I  V  D  L  V  S  E   200

601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201  L  K  K  D  V  L  M  V  L  V  N  Y  I  Y  F  K  A  L  W  E   220

661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTNTATGTTGATGAGAACACAACA  720
221  K  P  F  I  S  S  R  T  T  P  K  D  F  Y  V  D  E  N  T  T   240

721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241  V  R  V  P  M  M  L  Q  D  Q  E  H  H  W  Y  L  H  D  R  Y   260

781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261  L  P  C  S  V  L  R  M  D  Y  K  G  D  A  T  V  F  F  I  L   280
```

FIG. 36B

```
841  CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
281  P  N  Q  G  K  M  R  E  I  E  E  V  L  T  P  E  M  L  M  R    300

901  TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
301  W  N  N  L  L  R  K  R  N  F  Y  K  K  L  E  L  H  L  P  K    320

961  TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT  1020
321  F  S  I  S  G  S  Y  V  L  D  Q  I  L  P  R  L  G  F  T  D    340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC  1080
341  L  F  S  K  W  A  D  L  S  G  I  T  K  Q  Q  K  L  E  A  S    360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC  1140
361  K  S  F  H  K  A  T  L  D  V  D  E  A  G  T  E  A  A  A  A    380

1141 ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC  1200
381  T  T  F  A  I  K  F  F  S  A  Q  T  N  R  H  I  L  R  F  N    400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG  1260
401  R  P  F  L  V  V  I  F  S  T  S  T  Q  S  V  L  F  L  G  K    420

1261 GTCGTCGACCCCACGAAACCATAG  1284
421  V  V  D  P  T  K  P  *    428
```

FIG. 37A

```
   1  CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTTAGTCTA   60

  61  GGGAAAGTCATTCAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTG  120
   1                                          M  S  S  S  S  W      6

 121  GCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACCATTGAGGAACAGGCCAA  180
   7   L  L  L  S  L  V  A  V  T  A  A  Q  S  T  I  E  E  Q  A  K   26

 181  GACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC  240
  27   T  F  L  D  K  F  N  H  E  A  E  D  L  F  Y  Q  S  S  L  A   46

 241  TTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG  300
  47   S  W  N  N  Y  N  T  N  I  T  E  E  N  V  Q  N  M  N  N  A  G   66

 301  GGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA  360
  67   D  K  W  S  A  F  L  K  E  Q  S  T  L  A  Q  M  Y  P  L  Q   86

 361  AGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC  420
  87   E  I  Q  N  L  T  V  K  L  Q  L  Q  A  L  Q  Q  N  G  S  S  106

 421  AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT  480
 107   V  L  S  E  D  K  S  K  R  L  N  T  I  L  N  T  M  S  T  I  126

 481  CTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC  540
 127   Y  S  T  G  K  V  C  N  P  D  N  P  Q  E  C  L  L  L  E  P  146

 541  AGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA  600
 147   G  L  N  E  I  M  A  N  S  L  D  Y  N  E  R  L  W  A  W  E  166

 601  AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT  660
 167   S  W  R  S  E  V  G  K  Q  L  R  P  L  Y  E  E  Y  V  V  L  186

 661  GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA  720
 187   K  N  E  M  A  R  A  N  H  Y  E  D  Y  G  D  Y  W  R  G  D  206

 721  CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGT  780
 207   Y  E  V  N  G  V  D  G  Y  D  Y  S  R  G  Q  L  I  E  D  V  226

 781  GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC  840
 227   E  H  T  F  E  E  I  K  P  L  Y  E  H  L  H  A  Y  V  R  A  246

 841  AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT  900
 247   K  L  M  N  A  Y  P  S  Y  I  S  P  I  G  C  L  P  A  H  L  266
```

FIG. 37B

```
901  GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCCTTTGG  960
267    L  G  D  M  W  G  R  F  W  T  N  L  Y  S  L  T  V  P  F  G  286

961  ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG  1020
287    Q  K  P  N  I  D  V  T  D  A  M  V  D  Q  A  W  D  A  Q  R  306

1021 AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGG  1080
307    I  F  K  E  A  E  K  F  F  V  S  V  G  L  P  N  M  T  Q  G  326

1081 ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAGAAAGCAGTCTGCCATCC  1140
327    F  W  E  N  S  M  L  T  D  P  G  N  V  Q  K  A  V  C  H  P  346

1141 CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT  1200
347    T  A  W  D  L  G  K  G  D  F  R  I  L  M  C  T  K  V  T  M  366

1201 GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC  1260
367    D  D  F  L  T  A  H  H  E  M  G  H  I  Q  Y  D  M  A  Y  A  386

1261 TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGA  1320
387    A  Q  P  F  L  L  R  N  G  A  N  E  G  F  H  E  A  V  G  E  406

1321 AATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCACC  1380
407    I  M  S  L  S  A  A  T  P  K  H  L  K  S  I  G  L  L  S  P  426

1381 CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT  1440
427    D  F  Q  E  D  N  E  T  E  I  N  F  L  L  K  Q  A  L  T  I  446

1441 TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG  1500
447    V  G  T  L  P  F  T  Y  M  L  E  K  W  R  W  M  V  F  K  G  466

1501 GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG  1560
467    E  I  P  K  D  Q  W  M  K  K  W  W  E  M  K  R  E  I  V  G  486

1561 GGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGT  1620
487    V  V  E  P  V  P  H  D  E  T  Y  C  D  P  A  S  L  F  H  V  506

1621 TTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTTTACCAATTCCAGTTTCA  1680
507    S  N  D  Y  S  F  I  R  Y  Y  T  R  T  L  Y  Q  F  Q  F  Q  526

1681 AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA  1740
527    E  A  L  C  Q  A  A  K  H  E  G  P  L  H  K  C  D  I  S  N  546
```

FIG. 37C

```
1741  CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCTG  1800
 547   S  T  E  A  G  Q  K  L  F  N  M  L  R  L  G  K  S  E  P  W   566

1801  GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA  1860
 567   T  L  A  L  E  N  V  V  G  A  K  N  M  N  V  R  P  L  L  N   586

1861  CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATG  1920
 587   Y  F  E  P  L  F  T  W  L  K  D  Q  N  K  N  S  F  V  G  W   606

1921  GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC  1980
 607   S  T  D  W  S  P  Y  A  D  Q  S  I  K  V  R  I  S  L  K  S   626

1981  AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC  2040
 627   A  L  G  D  K  A  Y  E  W  N  D  N  E  M  Y  L  F  R  S  S   646

2041  TGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGG  2100
 647   V  A  Y  A  M  R  Q  Y  F  L  K  V  K  N  Q  M  I  L  F  G   666

2101  GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCAC  2160
 667   E  E  D  V  R  V  A  N  L  K  P  R  I  S  F  N  F  F  V  T   686

2161  TGCACCTAAAAACGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGAT  2220
 687   A  P  K  N  V  S  D  I  I  P  R  T  E  V  E  K  A  I  R  M   706

2221  GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG  2280
 707   S  R  S  R  I  N  D  A  F  R  L  N  D  N  S  L  E  F  L  G   726

2281  GATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTT  2340
 727   I  Q  P  T  L  G  P  P  N  Q  P  P  V  S  I  W  L  I  V  F   746

2341  TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG  2400
 747   G  V  V  M  G  V  I  V  V  G  I  V  I  L  I  F  T  G  I  R   766

2401  AGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT  2460
 767   D  R  K  K  K  N  K  A  R  S  G  E  N  P  Y  A  S  I  D  I   786

2461  TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTTTTA  2520
 787   S  K  G  E  N  N  P  G  F  Q  N  T  D  D  V  Q  T  S  F  *   806

2521  GAAAAATCTATGTTTTTCCTCTTGAGGTGATTTTGTTGTATGTAAATGTTAATTTCATGG  2580

2581  TATAGAAAATATAAGATGATAAAGATATCATTAAATGTCAAAACTATGACTCTGTTCAGA  2640
```

FIG. 37D

```
2641  AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC  2700

2701  AGTATTTATTTCTGTCTCTGGATTTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGTAT  2760

2761  TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTCAGGGATAATCTAAAT  2820

2821  GTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTTG  2880

2881  GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAACTGGTGTAGC  2940

2941  TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA  3000

3001  CATGCTTTCTTCACAGTAACTCAGTTCAAGTACTATGGTGATTTGCCTACAGTGATGTTT  3060

3061  GGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG  3120

3121  GTAGAGGACATTGCTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA  3180

3181  AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAAACTCATTTCTAC  3240

3241  TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACTGTATGTTCACCCTCTGAAGTGGGT  3300

3301  ACCCAGTCTCTTAAATCTTTTGTATTTGCTCACAGTGTTTGAGCAGTGCTGAGCACAAAG  3360

3361  CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAA  3405
```

FIG. 38A

```
   1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTN GTGAGGNCTC CGTGCCCACC 60
   1 M  F  S  P   W  K  I   S  M  F   L  S  V  X   E  X  S   V  P  T  20

  61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
  21 T  A  S  F   S  A  D   M  L  N   V  T  L  Q   G  P  T   L  N  G  40

 121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
  41 T  F  A  Q   S  K  C   P  Q  V   E  W  L  G   W  L  N   T  I  Q  60

 181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
  61 P  P  F  L   W  V  L   F  V  L   A  T  L  E   N  I  F   V  L  S  80

 241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
  81 V  F  C  L   H  K  S   S  C  T   V  A  E  I   Y  L  G   N  L  A  100

 301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
 101 A  A  D  L   I  L  A   C  G  L   P  F  W  A   I  T  I   S  N  N  120

 361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
 121 F  D  W  L   F  G  E   T  L  C   R  V  V  N   A  I  I   S  M  N  140

 421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
 141 L  Y  S  S   I  C  F   L  M  L   V  S  I  D   R  Y  L   A  L  V  160

 481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
 161 K  T  M  S   M  G  R   M  R  G   V  R  W  A   K  L  Y   S  L  V  180

 541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
 181 I  W  G  C   T  L  L   L  S  S   P  M  L  V   F  R  T   M  K  E  200

 601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
 201 Y  S  D  E   G  H  N   V  T  A   C  V  I  S   Y  P  S   L  I  W  220

 661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
 221 E  V  F  T   N  M  L   L  N  V   V  G  F  L   L  P  L   S  V  I  240

 721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
 241 T  F  C  T   M  Q  I   M  Q  V   L  R  N  N   E  M  Q   K  F  K  260

 781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
 261 E  I  Q  T   E  R  R   A  T  V   L  V  L  V   V  L  L   L  F  I  280

 841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I  C  W  L   P  F  Q   I  S  T   F  L  D  T   L  H  R   L  G  I  300
```

FIG. 38B

```
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GANGTAATCA CACAGATCGC CTCCTTCATG 960
301 L  S  S  C   Q  D  E   R  I  I   D  V  I  T   Q  I  A   S  F  M  320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
321 A  Y  S  N   S  C  L   N  P  L   V  Y  V  I   V  G  K   R  F  R  340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG NGGGCTGCAG GTCAGAACCC 1080
341 K  K  S  W   E  V  Y   Q  G  V   C  Q  K  X   G  C  R   S  E  P  360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
361 I  Q  M  E   N  S  M   G  T  L   R  T  S  I   S  V  E   R  Q  I  380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
381 H  K  L  Q   D  W  A   G  S  R   Q  *                             391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

FIG. 38C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 38D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733

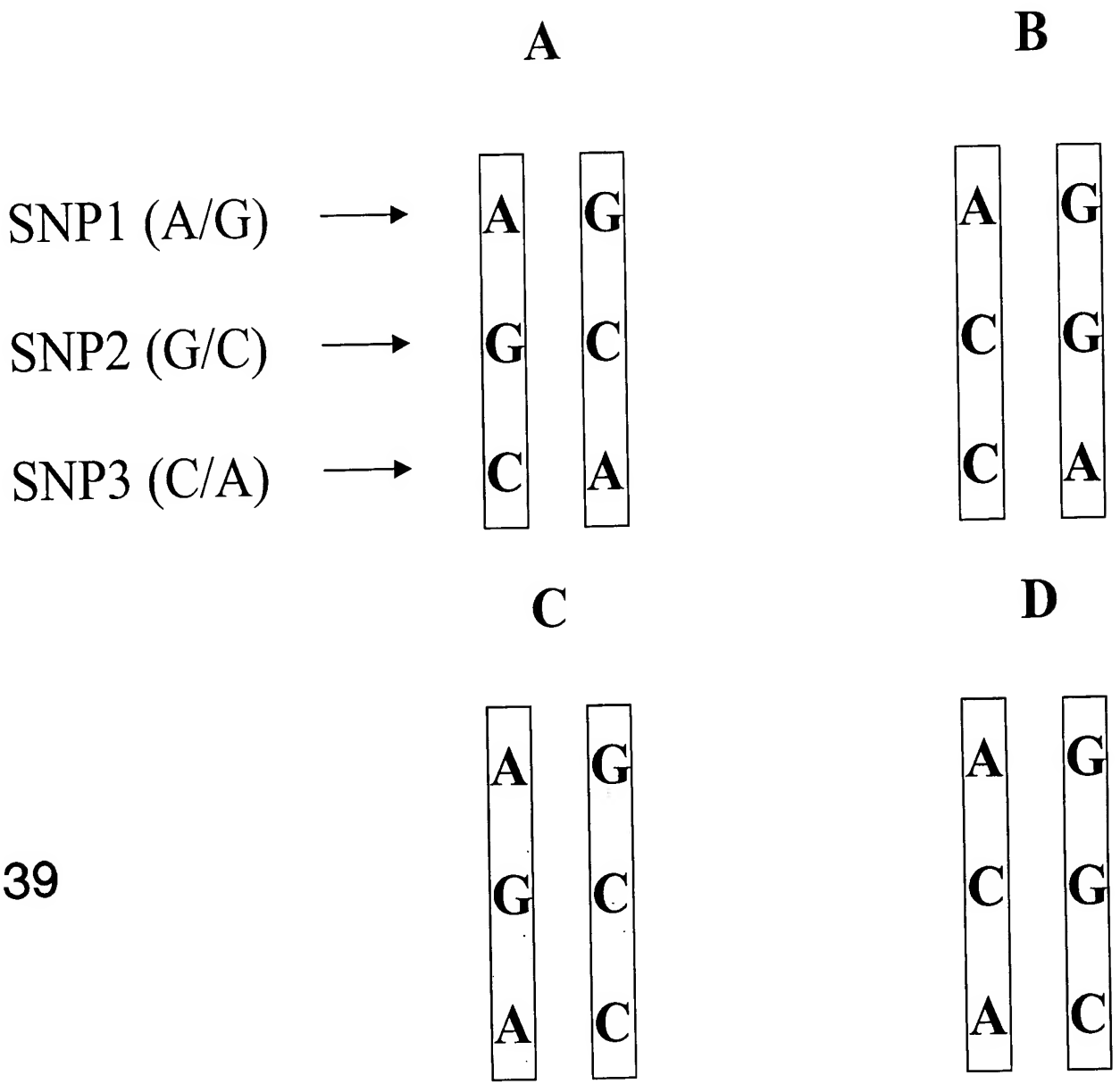

FIG. 39

FIG. 40

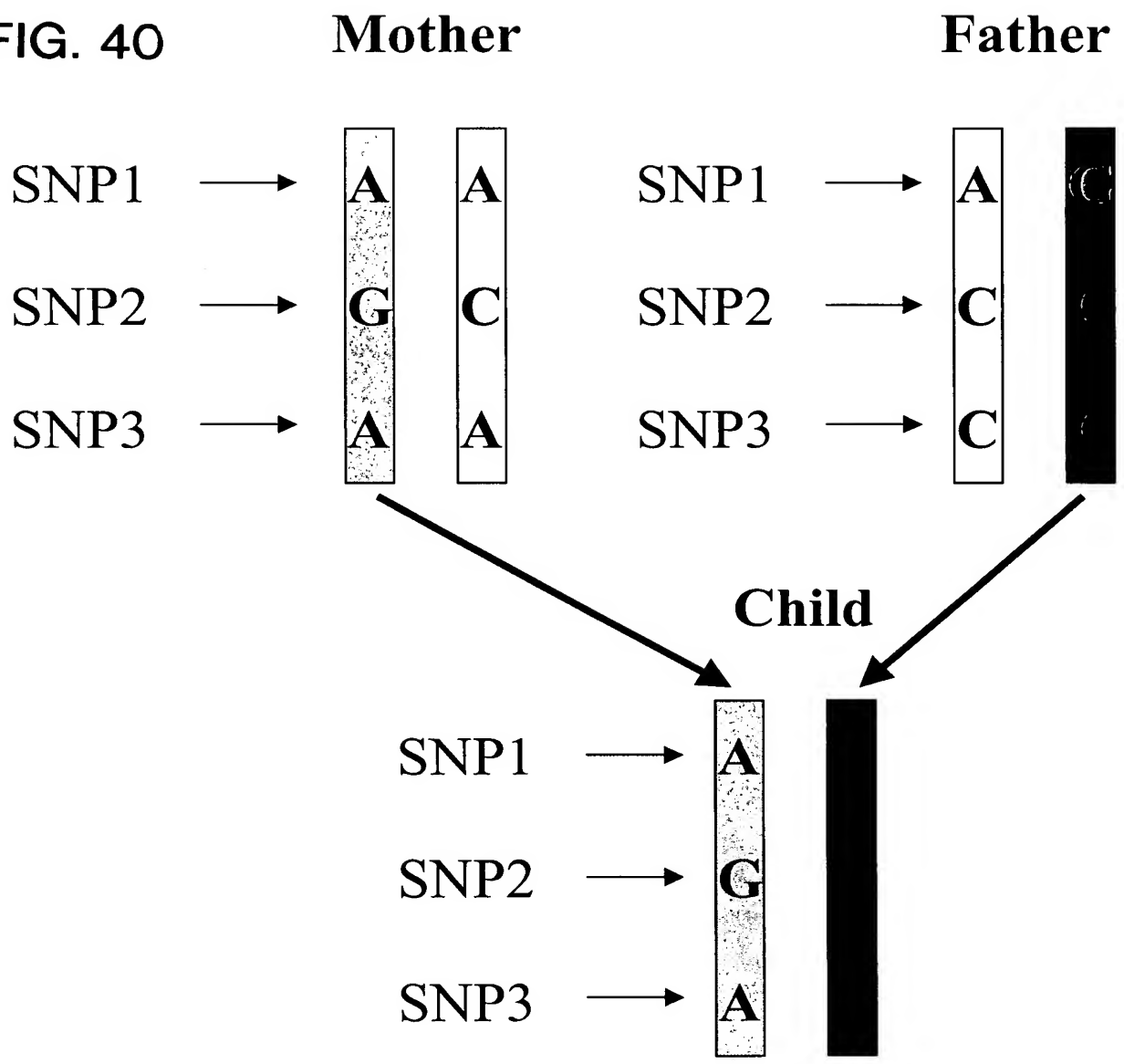
Mother
Father
SNP1
SNP2
SNP3
A
A
G
C
A
A
SNP1
SNP2
SNP3
A
C
C
Child
SNP1
SNP2
SNP3
A
G
A

FIG. 41A

```
   1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC  60

  61 TGCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120

 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180

 181 AGGCCTGAAG GAACAGGCCG GGGAAGGAGC CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240

 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
   1                              M  A  R  A  H  W  G  C  C  P  W  L  12

 301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
  13 V  L  L  C  A  C  A  W  G  H  T  K  P  L  D  L  G  G  Q  D  32

 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
  33 V  R  N  C  S  T  N  P  P  Y  L  P  V  T  V  V  N  T  T  M  52

 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
  53 S  L  T  A  L  R  Q  Q  M  Q  T  Q  N  L  S  A  Y  I  I  P  72

 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
  73 G  T  D  A  H  M  N  E  Y  I  G  Q  H  D  E  R  R  A  W  I  92

 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
  93 T  G  F  T  G  S  A  G  T  A  V  V  T  M  K  K  A  A  V  W  112

 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T  D  S  R  Y  W  T  Q  A  E  R  Q  M  D  C  N  W  E  L  H  132

 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC TGCTGGAGGG 720
 133 K  E  V  G  T  T  P  I  V  T  W  L  L  T  E  I  P  A  G  G  152

 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R  V  G  F  D  P  F  L  L  S  I  D  T  W  E  S  Y  D  L  A  172

 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L  Q  G  S  N  R  Q  L  V  S  I  T  T  N  L  V  D  L  V  W  192

 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
 193 G  S  E  R  P  P  V  P  N  Q  P  I  Y  A  L  Q  E  A  F  T  212

 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G  S  T  W  Q  E  K  V  S  G  V  R  S  Q  M  Q  K  H  Q  K  232
```

FIG. 41B

```
961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V  P  T  A  V  L  L  S  A  L  E  E  T  A  W  L  F  N  L  R  252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
253 A  S  D  I  P  Y  N  P  F  F  Y  S  Y  T  L  L  T  D  S  S  272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
273 I  R  L  F  A  N  K  S  R  F  S  S  E  T  L  S  Y  L  N  S  292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
293 S  C  T  G  P  M  C  V  Q  I  E  D  Y  S  Q  V  R  D  S  I  312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q  A  Y  S  L  G  D  V  R  I  W  I  G  T  S  Y  T  M  Y  G  332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I  Y  E  M  I  P  R  E  K  L  V  T  D  T  Y  S  P  V  M  M  352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T  K  A  V  K  N  S  K  E  Q  A  L  L  K  A  S  H  V  R  D  372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A  V  A  V  I  R  Y  L  V  W  L  E  K  N  V  P  K  G  T  V  392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
393 D  E  F  S  G  A  E  I  V  D  K  F  R  G  E  E  Q  F  S  S  412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G  P  S  F  E  T  I  S  A  S  G  L  N  A  A  L  A  H  Y  S  432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
433 P  T  K  E  L  N  R  K  L  S  S  D  E  M  Y  L  L  D  S  G  452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
453 G  Q  Y  W  D  G  T  T  D  I  T  R  T  V  H  W  G  T  P  S  472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A  F  Q  K  E  A  Y  T  R  V  L  I  G  N  I  D  L  S  R  L  492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
493 I  F  P  A  A  T  S  G  R  M  V  E  A  F  A  R  R  A  L  W  512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D  A  G  L  N  Y  G  H  G  T  G  H  G  I  G  N  F  L  C  V  532
```

FIG. 41C

```
1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H  E  W  P   V  G  F   Q  S  N   N  I  A  M   A  K  G   M  F  T   552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S  I  E  P   G  Y  Y   K  D  G   E  F  G  I   R  L  E   D  V  A   572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L  V  V  E   A  K  T   K  Y  P   G  E  L  P   D  L  V   V  S  F   592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593 V  P  Y  D   R  N  L   I  D  V   S  L  L  S   P  E  H   L  Q  Y   612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L  N  R  Y   Y  Q  T   I  R  E   K  V  G  P   E  L  Q   R  R  Q   632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L  L  E  E   F  E  W   L  Q  Q   H  T  E  P   L  A  A   R  A  P   652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D  T  A  S   W  A  S   V  L  V   V  S  T  L   A  I  L   G  W  S   672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V  *                                                              673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940
```

FIG. 41D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428

FIG. 42A

```
 1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1       M  A  S  S  W  P  P  L  E  L  Q  S  S  N  Q  S  Q  L  18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F  P  Q  N  A  T  A  C  D  N  A  P  E  A  W  D  L  L  H  R  38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V  L  P  T  F  I  I  S  I  C  F  F  G  L  L  G  N  L  F  V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L  L  V  F  L  L  P  R  R  Q  L  N  V  A  E  I  Y  L  A  N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L  A  A  S  D  L  V  F  V  L  G  L  P  F  W  A  E  N  I  W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
99 N  Q  F  N  W  P  F  G  A  L  L  C  R  V  I  N  G  V  I  K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A  N  L  F  I  S  I  F  L  V  V  A  I  S  Q  D  R  Y  R  V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L  V  H  P  M  A  S  G  R  Q  Q  R  R  R  Q  A  R  V  T  C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V  L  I  W  V  V  G  G  L  L  S  I  P  T  F  L  L  R  S  I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q  A  V  P  D  L  N  I  T  A  C  I  L  L  L  P  H  E  A  W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H  F  A  R  I  V  E  L  N  I  L  G  F  L  L  P  L  A  A  I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V  F  F  N  Y  H  I  L  A  S  L  R  T  R  E  E  V  S  R  T  238

721 AGAGTGCAGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R  V  Q  G  P  K  D  S  K  T  T  A  L  I  L  T  L  V  V  A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F  L  V  C  W  A  P  Y  H  F  F  A  F  L  E  F  L  F  Q  V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q  A  V  R  G  C  F  W  E  D  F  I  D  L  G  L  Q  L  A  N  298
```

FIG. 42B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F  F  A  F   T  N  S   S  L  N   P  V  I  Y   V  F  V   G  R  L   318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F  R  T  K   V  W  E   L  Y  K   Q  C  T  P   K  S  L   A  P  I   338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S  S  S  H   R  K  E   I  F  Q   L  F  W  R   N  *                353

1081 CC 1082
```

FIG. 43A

```
 1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGCCTC CGTGCCCACC 60
 1 M  F  S  P  W  K  I  S  M  F  L  S  V  R  E  A  S  V  P  T  20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G  40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q  60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
 61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S  80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  V  L  L  L  F  I  280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

FIG. 43B

```
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
301 L  S  S  C   Q  D  E   R  I  I   D  V  I  T   Q  I  A   S  F  M   320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
321 A  Y  S  N   S  C  L   N  P  L   V  Y  V  I   V  G  K   R  F  R   340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
341 K  K  S  W   E  V  Y   Q  G  V   C  Q  K  G   G  C  R   S  E  P   360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
361 I  Q  M  E   N  S  M   G  T  L   R  T  S  I   S  V  E   R  Q  I   380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
381 H  K  L  Q   D  W  A   G  S  R   Q  *                             391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

FIG. 43C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 43D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733

FIG. 44A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1  M  H  L  I  D  Y  L  L  L  L  L  V  G  L  L  A  L  S  H  G    20

 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21  Q  L  H  V  E  H  D  G  E  S  C  S  N  S  S  H  Q  Q  I  L    40

121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41  E  T  G  E  G  S  P  S  L  K  I  A  P  A  N  A  D  F  A  F    60

181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61  R  F  Y  Y  L  I  A  S  E  T  P  G  K  N  I  F  F  S  P  L    80

241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81  S  I  S  A  A  Y  A  M  L  S  L  G  A  C  S  H  S  R  S  Q   100

301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101  I  L  E  G  L  G  F  N  L  T  E  L  S  E  S  D  V  H  R  G   120

361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC  420
121  F  Q  H  L  L  H  T  L  N  L  P  G  H  G  L  E  T  R  V  G   140

421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141  S  A  L  F  L  S  H  N  L  K  F  L  A  K  F  L  N  D  T  M   160

481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161  A  V  Y  E  A  K  L  F  H  T  N  F  Y  D  T  V  G  T  I  Q   180

541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG  600
181  L  I  N  D  H  V  K  K  E  T  R  G  K  I  V  D  L  V  S  E   200

601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201  L  K  K  D  V  L  M  V  L  V  N  Y  I  Y  F  K  A  L  W  E   220

661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA  720
221  K  P  F  I  S  S  R  T  T  P  K  D  F  Y  V  D  E  N  T  T   240

721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241  V  R  V  P  M  M  L  Q  D  Q  E  H  H  W  Y  L  H  D  R  Y   260

781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261  L  P  C  S  V  L  R  M  D  Y  K  G  D  A  T  V  F  F  I  L   280
```

FIG. 44B

```
841  CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
281  P  N  Q  G  K  M  R  E  I  E  E  V  L  T  P  E  M  L  M  R    300

901  TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
301  W  N  N  L  L  R  K  R  N  F  Y  K  K  L  E  L  H  L  P  K    320

961  TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT   1020
321  F  S  I  S  G  S  Y  V  L  D  Q  I  L  P  R  L  G  F  T  D    340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC   1080
341  L  F  S  K  W  A  D  L  S  G  I  T  K  Q  Q  K  L  E  A  S    360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   1140
361  K  S  F  H  K  A  T  L  D  V  D  E  A  G  T  E  A  A  A  A    380

1141 ACGACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC   1200
381  T  T  F  A  I  K  F  F  S  A  Q  T  N  R  H  I  L  R  F  N    400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG   1260
401  R  P  F  L  V  V  I  F  S  T  S  T  Q  S  V  L  F  L  G  K    420

1261 GTCGTCGACCCCACGAAACCATAG  1284
421  V  V  D  P  T  K  P  *     428
```

FIG. 45A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1  M  H  L  I  D  Y  L  L  L  L  L  V  G  L  L  A  L  S  H  G    20

 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21  Q  L  H  V  E  H  D  G  E  S  C  S  N  S  S  H  Q  Q  I  L    40

121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41  E  T  G  E  G  S  P  S  L  K  I  A  P  A  N  A  D  F  A  F    60

181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61  R  F  Y  Y  L  I  A  S  E  T  P  G  K  N  I  F  F  S  P  L    80

241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81  S  I  S  A  A  Y  A  M  L  S  L  G  A  C  S  H  S  R  S  Q   100

301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101  I  L  E  G  L  G  F  N  L  T  E  L  S  E  S  D  V  H  R  G   120

361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACATGCGTGGGC  420
121  F  Q  H  L  L  H  T  L  N  L  P  G  H  G  L  E  T  C  V  G   140

421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141  S  A  L  F  L  S  H  N  L  K  F  L  A  K  F  L  N  D  T  M   160

481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161  A  V  Y  E  A  K  L  F  H  T  N  F  Y  D  T  V  G  T  I  Q   180

541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG  600
181  L  I  N  D  H  V  K  K  E  T  R  G  K  I  V  D  L  V  S  E   200

601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201  L  K  K  D  V  L  M  V  L  V  N  Y  I  Y  F  K  A  L  W  E   220

661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA  720
221  K  P  F  I  S  S  R  T  T  P  K  D  F  Y  V  D  E  N  T  T   240

721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241  V  R  V  P  M  M  L  Q  D  Q  E  H  H  W  Y  L  H  D  R  Y   260

781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261  L  P  C  S  V  L  R  M  D  Y  K  G  D  A  T  V  F  F  I  L   280
```

FIG. 45B

```
 841  CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
 281  P  N  Q  G  K  M  R  E  I  E  E  V  L  T  P  E  M  L  M  R    300

 901  TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
 301  W  N  N  L  L  R  K  R  N  F  Y  K  K  L  E  L  H  L  P  K    320

 961  TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT   1020
 321  F  S  I  S  G  S  Y  V  L  D  Q  I  L  P  R  L  G  F  T  D    340

1021  CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC   1080
 341  L  F  S  K  W  A  D  L  S  G  I  T  K  Q  Q  K  L  E  A  S    360

1081  AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   1140
 361  K  S  F  H  K  A  T  L  D  V  D  E  A  G  T  E  A  A  A  A    380

1141  ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC   1200
 381  T  T  F  A  I  K  F  F  S  A  Q  T  N  R  H  I  L  R  F  N    400

1201  CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG   1260
 401  R  P  F  L  V  V  I  F  S  T  S  T  Q  S  V  L  F  L  G  K    420

1261  GTCGTCGACCCCACGAAACCATAG  1284
 421  V  V  D  P  T  K  P  *    428
```

FIG. 46A

```
   1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC  60

  61 TGCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120

 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180

 181 AGGCCTGAAG GAACAGGCCG GGGAAGGAGC CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240

 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
   1                              M  A  R  A  H  W  G  C  C  P  W  L  12

 301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
  13 V  L  L  C  A  C  A  W  G  H  T  K  P  L  D  L  G  G  Q  D  32

 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
  33 V  R  N  C  S  T  N  P  P  Y  L  P  V  T  V  V  N  T  T  M  52

 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
  53 S  L  T  A  L  R  Q  Q  M  Q  T  Q  N  L  S  A  Y  I  I  P  72

 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
  73 G  T  D  A  H  M  N  E  Y  I  G  Q  H  D  E  R  R  A  W  I  92

 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
  93 T  G  F  T  G  S  A  G  T  A  V  V  T  M  K  K  A  A  V  W  112

 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T  D  S  R  Y  W  T  Q  A  E  R  Q  M  D  C  N  W  E  L  H  132

 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC NGCTGGAGGG 720
 133 K  E  V  G  T  T  P  I  V  T  W  L  L  T  E  I  P  A  G  G  152

 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R  V  G  F  D  P  F  L  L  S  I  D  T  W  E  S  Y  D  L  A  172

 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L  Q  G  S  N  R  Q  L  V  S  I  T  T  N  L  V  D  L  V  W  192

 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
 193 G  S  E  R  P  P  V  P  N  Q  P  I  Y  A  L  Q  E  A  F  T  212

 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G  S  T  W  Q  E  K  V  S  G  V  R  S  Q  M  Q  K  H  Q  K  232
```

FIG. 46B

```
 961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V  P  T  A   V  L  L   S  A  L   E  E  T  A   W  L  F   N  L  R   252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A  S  D  I   P  Y  N   P  F  F   Y  S  Y  T   L  L  T   D  S  S   272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
 273 I  R  L  F   A  N  K   S  R  F   S  S  E  T   L  S  Y   L  N  S   292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S  C  T  G   P  M  C   V  Q  I   E  D  Y  S   Q  V  R   D  S  I   312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q  A  Y  S   L  G  D   V  R  I   W  I  G  T   S  Y  T   M  Y  G   332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I  Y  E  M   I  P  R   E  K  L   V  T  D  T   Y  S  P   V  M  M   352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
 353 T  K  A  V   K  N  S   K  E  Q   A  L  L  K   A  S  H   V  R  D   372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A  V  A  V   I  R  Y   L  V  W   L  E  K  N   V  P  K   G  T  V   392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
 393 D  E  F  S   G  A  E   I  V  D   K  F  R  G   E  E  Q   F  S  S   412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G  P  S  F   E  T  I   S  A  S   G  L  N  A   A  L  A   H  Y  S   432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P  T  K  E   L  N  R   K  L  S   S  D  E  M   Y  L  L   D  S  G   452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
 453 G  Q  Y  W   D  G  T   T  D  I   T  R  T  V   H  W  G   T  P  S   472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A  F  Q  K   E  A  Y   T  R  V   L  I  G  N   I  D  L   S  R  L   492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I  F  P  A   A  T  S   G  R  M   V  E  A  F   A  R  R   A  L  W   512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D  A  G  L   N  Y  G   H  G  T   G  H  G  I   G  N  F   L  C  V   532
```

FIG. 46C

```
1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H  E  W  P   V  G  F   Q  S  N   N  I  A  M   A  K  G   M  F  T   552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S  I  E  P   G  Y  Y   K  D  G   E  F  G  I   R  L  E   D  V  A   572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L  V  V  E   A  K  T   K  Y  P   G  E  L  P   D  L  V   V  S  F   592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCNGAGCA TCTCCAGTAC 2100
 593 V  P  Y  D   R  N  L   I  D  V   S  L  L  S   P  E  H   L  Q  Y   612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L  N  R  Y   Y  Q  T   I  R  E   K  V  G  P   E  L  Q   R  R  Q   632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L  L  E  E   F  E  W   L  Q  Q   H  T  E  P   L  A  A   R  A  P   652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D  T  A  S   W  A  S   V  L  V   V  S  T  L   A  I  L   G  W  S   672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V  *                                                              673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940
```

FIG. 46D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428

Table III

Gene Name	Coriell DNA Panel(s)	Amplicon No.	Total SNPs	Missense	Silent	UTR	Intronic
Aminopeptidase P (XPNPEP2)	24 + 47 (55AA) +12pt	24	30	0	2	7	21
Bradykinin B1 receptor (BDKRB1)	24+ 95 (8AA, 103 CAU) +12pt	7	14	2	5	3	4
Bradykinin B2 receptor (BDKRB2)	24 (8AA) +12pt	12	36	3	2	14	17
NK1 tachykinin receptor (TACR1)	24 (8AA) +12pt	7	9	0	3	3	3
C1 esterase inhibitor (C1NH)	24 (8AA) +12pt	10	6	2	2	0	2
Kallikrein 1 (KLK1)	7 (7AA) +12pt	5	6	1	1	2	2
Protease Inhibitor 4 (PI4)	7 (7AA) +12pt	8	12	1	3	1	7
Angiotensin Converting Enzyme 2 (ACE2)	7 (7AA) +12pt	20	9	0	0	0	9
Totals:			122	9	18	30	65

Table IV (1 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	FLANK_SEQ (REF / ALT)	FLANK_SEQ REF (SEQ ID NO:)	FLANK_SEQ ALT (SEQ ID NO:)	REF_SEQ_ID	REF_SEQ_POS	REF_NT	ALT_NT	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	CDNA_SEQ_ID	CDNA_SEQ_POS
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	1	127	GCTGTCTCC [C/G] GAGCATGTG	37	100	AL023653.1	82696	C	G	Exon20	Silent	0	CCC	CCG	U90724.1	2085
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	4	535	AGAACAGTC [T/C] AGTGTTACA	38	101	AL023653.1	80150	C	T	Intron3	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s3	5	224	CTCACCACC [C/T] TCCCCCAAG	39	102	AL023653.1	74483	T	C	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s4	5	392	AGGCCTCAG [T/C] CCAAGCTGA	40	103	AL023653.1	74651	C	T	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s5	6	432	CGGGCCCCA [G/A] CCCTCACTC	41	104	AL023653.1	54549	T	C	Intron1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s6	7	258	TAATAAAAG [A/G] GGGGTGGCC	42	105	AL023653.1	76521	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	10	461	AAAAGCAGC [G/A] AAACCCTTT	43	106	AL023653.1	65566	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	13	273	CACAGGGG [C/T] GTTTTCAGA	44	107	AL023653.1	68266	A	G	Intron10	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	13	324	TTTGCCACC [A/G] TTTCGTGGC	45	108	AL023653.1	68236	T	C	Intron10	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	14	856	AGCATGCAC [C/G] TGAGTCACC	46	109	AL023653.1	63068	C	G	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	15	187	AGGT [T/C] CTCCACCA	47	110	AL023653.1	71620	C	T	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	15	194	CCTCCA [C/T] CAAGGCC	48	111	AL023653.1	71627	C	T	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	15	218	GACCCAGT [G/A] CAGGGTTAG	49	112	AL023653.1	71651	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	8	221	TTTCCCCGG [G/C] CTCTTCCTT	50	113	AL023653.1	54356	G	C	Exon1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	6	243	GCCTTTCCT [A/G] GGCTCGAGC	51	114	AL023653.1	54334	C	T	Exon1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s16	14	139	AATATTTAA [C/T] GCTGATCTG	52	115	AL023653.1	66924	A	G	Intron8	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s17	22	809	GAAAGGA [A/C] GACATA	53	116	AL023653.1	77205	T	G	Intron17	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s18	22	964	AGGATTGGC [T/G] CTGGCTTTT	54	117	AL023653.1	77052	A	C	Intron17	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s19	26	195	TGGAGGA [C/T] GGGAGGAG	55	118	AL023653.1	75689	G	A	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s20	27	306	TGGCTT [A/G] GAGAGGCTG	56	119	AL023653.1	63489	A	G	Intron20	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s21	27	695	GGTCCCAGG [A/C] CCCAGGAAC	57	120	AL023653.1	63858	C	A	Exon21	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	28	710	TACCACACC [C/G] TGGGCCCC	58	121	AL023653.1	63926	C	G	Exon21	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	28	1369	GCATTCCAG [C/T] TCTTTCACC	59	122	AL023653.1	64585	C	T	Exon21	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s1	6	307	TGTGGGCC [G/A] GCTCTTCA	60	123	U48231.1	2207	G	A	Exon2	Missense	0	CGG	CAG	NM_000710.1	956
Bradykinin Receptor B1	BDKRB1	AE103s2	4	273	ATAAATGT [T/C] GGCAGCACT	61	124	U48231.1	1380	G	A	Exon2	Silent	0	CCG	CCA	NM_000710.1	129
Bradykinin Receptor B1	BDKRB1	AE103s3	7	958	ACAAAGAAT [T/C] GATAAGAAA	62	125	U48231.1	2355	A	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s4	1	196	ACGGACTGA [G/A] ACCCTGTCT	63	126	U48231.1	230	C	T	Exon1	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s5	7	240	CAGTGGCCA [T/C] GCCTATAAT	64	127	U48231.1	3072	G	A	Exon3	Non-CDS	0				
Bradykinin Receptor B2	BDKRB2	AE104s1	10	86	GGCTCCCCC [C/G] GCCGCGCCC	65	128	AL355102.2	98426	C	G	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s2	10	87	GCGCCCCCC [A/G] CCGCGCCCA	66	129	AL355102.2	98427	A	G	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s3	10	462	AGGTCATG [T/A] TCCCCCTCT	67	130	AL355102.2	98802	T	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s4	10	542	GGGATGAGG [C/T] CTGGGGTGC	68	131	AL355102.2	98882	C	T	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s5	10	557	GTGCTGCCT [G/A] TGGGGACAG	69	132	AL355102.2	98897	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s6	10	717	AGGAC [A/G] CAGCACAGT	70	133	AL355102.2	99056	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s7	7	408	GTCCCACAA [C/G] CCCCCTGCT	71	134	AL355102.2	66369	G	C	Intron2	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s8	5	275	GCACAACCA [T/C] CTGTCCCTG	72	135	AL355102.2	62853	A	G	Exon3	Non-CDS	1			NM_000623.1	2002
Bradykinin Receptor B2	BDKRB2	AE104s9	5	390	TGAGGCATC [A/T] TTACGCAG	73	136	AL355102.2	62738	T	A	Exon3	Non-CDS	1			NM_000623.1	2117
Bradykinin Receptor B2	BDKRB2	AE104s10	5	527	AGGTGCTCA [C/T] TGGCTCCCT	74	137	AL355102.2	62601	A	G	Exon3	Non-CDS	1			NM_000623.1	2254
Bradykinin Receptor B2	BDKRB2	AE104s11	6	579	TGAGTCTT [T/G] CACAGGACA	75	138	AL355102.2	61132	T	G	Exon3	Non-CDS	1			NM_000623.1	3804
Bradykinin Receptor B2	BDKRB2	AE104s12	6	585	CTTTCACAG [G/T] ACAGATGT	76	139	AL355102.2	61136	G	T	Exon3	Non-CDS	1			NM_000623.1	3508
Bradykinin Receptor B2	BDKRB2	AE104s13	6	727	AGACCATCA [T/C] GTGCTCTGG	77	140	AL355102.2	61280	C	T	Exon3	Non-CDS	1			NM_000623.1	3456
Bradykinin Receptor B2	BDKRB2	AE104s14	6	482	ACCATTG [T/C] CATTGCT	78	141	AL355102.2	62290	C	T	Exon3	Non-CDS	1			NM_000623.1	2565
Bradykinin Receptor B2	BDKRB2	AE104s16	9	1010	TAAACAAAA [T/C] TTGCCTAG	79	142	AL355102.2	60403	G	A	3' Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s17	9	1072	CCATGCCAG [A/G] AACCTGGGG	80	143	AL355102.2	60341	C	T	3' Flank	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s1	1	614	CAACTTCTT [T/C] CCCATCGCC	81	144	AC007681.3	103665	A	G	Exon1	Silent	1	TTT	TTC	NM_001058.2	543
Tachykinin Receptor 1	TACR1	AE106s2	2	789	CAGGACCCA [T/G] ATGACACAG	82	145	AC007681.3	25759	G	T	Exon2	Silent	1	ATC	ATA	NM_001058.2	672
Tachykinin Receptor 1	TACR1	AE106s3	4	676	TTCTGCCTG [T/G] CCCCTGCT	83	146	AC007400.3	143458	T	G	Intron3	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s4	6	152	GAATGGGCT [T/C] TTGGGAAAA	84	147	AC007400.3	139028	T	C	Exon5	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s5	6	220	TTTGAGTCA [C/A] ACAGCATGA	85	148	AC007400.3	139096	C	A	Exon5	Non-CDS	1			NM_001058.2	1635
Tachykinin Receptor 1	TACR1	AE106s6	6	317	TGCAAGTCC [T/C] AGTGTGAGG	86	149	AC007400.3	139193	C	T	Exon5	Non-CDS	1			NM_001058.2	1538
Tachykinin Receptor 1	TACR1	AE106s7	6	511	GTCCAGGGA [C/T] GAGGGTGTG	87	150	AC007400.3	139387	C	T	Exon5	Silent	1	TCG	TCA	NM_001058.2	1344
C1 Esterase Inhibitor	C1NH	AE105s1	3	319	AAAGGACA [G/A] AGGGAAT	88	151	X54486.1	5755	G	A	Intron4	Non-CDS	0				
C1 Esterase Inhibitor	C1NH	AE105s2	5	158	ACTGTTAAG [G/A] TGCATCTCT	89	152	X54486.1	15193	A	G	Intron6	Non-CDS	0				
C1 Esterase Inhibitor	C1NH	AE105s3	5	366	CGACCAG [C/T] CAGGATATG	90	153	X54486.1	15401	C	T	Exon7	Silent	0	AGC	AGT	NM_000062.1	1278
C1 Esterase Inhibitor	C1NH	AE105s4	7	588	TGCTATTCG [T/C] TGAACCCAT	91	154	X54486.1	3493	T	C	Exon3	Missense	0	GTT	GCT	NM_000062.1	227
C1 Esterase Inhibitor	C1NH	AE105s5	7	897	CCTTCTCAG [C/G] AATGAAGAA	92	155	X54486.1	3802	C	G	Exon3	Missense	0	GCA	GGA	NM_000062.1	536
C1 Esterase Inhibitor	C1NH	AE105s6	8	276	TTCCTCTTC [A/G] TGCTCTGGG	93	156	X54486.1	18012	G	A	Exon8	Missense	0	GTG	ATG	NM_000062.1	1498
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	1	153	GGGCTTTTT [C/T] GCACTCATC	94	157	AF277050.1	4773	A	G	Exon4	Missense	0	AAA	GAA	NM_002257.1	592
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	1	299	CCCCATCCC [C/T] GCCTTGGGC	95	158	AF277050.1	4627	G	A	Intron3	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	2	805	TTGCCCACC [G/C] AGGAACCCG	96	159	AF277050.1	4532	G	C	Exon3	Missense	0	GAG	CAG	NM_002257.1	469
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s4	2	717	GGACTCCTG [C/T] GTCCAAGGG	97	160	AF277050.1	4644	C	T	Intron3	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s5	4	632	GGCATGAGA [C/T] TGACACAGC	98	161	AF277050.1	5693	A	G	3' Flank	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s6	4	697	TGGAAAGAT [G/A] GGTGATGGC	99	162	AF277050.1	5628	T	C	3' Flank	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s6	1	67	TGTCATCAA [T/C] GGGGTCAT	579	611	U48231.1	1509	C	T	Exon3	Silent	0	AAC	AAT	NM_000710.1	348
Bradykinin Receptor B1	BDKRB1	AE103s7	1	181	CGGCGGAG [G/A] CAGGCCCGG	580	612	U48231.1	1713	G	A	Exon3	Silent	0	AGG	AGA	NM_000710.1	462
Bradykinin Receptor B1	BDKRB1	AE103s8	1	296	GCCTGCATC [C/G] TGCTCCTC	581	613	U48231.1	1828	C	G	Exon3	Missense	0	CTG	GTG	NM_000710.1	577
Bradykinin Receptor B1	BDKRB1	AE103s9	2	136	ACGCGGGA [G/A] GAGGTCAGA	582	614	U48231.1	1956	G	A	Exon3	Silent	0	GAG	GAA	NM_000710.1	705
Bradykinin Receptor B2	BDKRB2	AE104s18	7	202	TGGAGAATG [C/A] GTGTATTT	583	615	AL355102.2	68174	G	T	Intron1 c	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s19	7	339	TGTCTGTT [C/T] GTGAGGACT	584	616	AL355102.2	68037	G	A	Exon2	Missense	1	CGT	TGT	NM_000623.1	40
Bradykinin Receptor B2	BDKRB2	AE104s20	2	271	CCTTCCTTC [C/A] GAAGAGAAC	585	617	AL355102.2	101076	A	C	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s21	3	408	AAACACCCG [C/T] ACCCAGGAA	586	618	AL355102.2	100859	A	G	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s22	3	463	GTACGTGGC [G/A] TACAAAGAA	587	619	AL355102.2	100804	T	C	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s23	3	886	ATGACATCA [T/C] TACCCAGCC	588	620	AL355102.2	100391	G	A	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s24	4	918	CATCATCGA [T/C] GTAATCACA	589	621	AL355102.2	63922	A	G	Exon3	Silent	1	GAT	GAC	NM_000623.1	933
Bradykinin Receptor B2	BDKRB2	AE104s25	4	1046	GCCAGAAAG [G/A] GGGCTGCAG	590	622	AL355102.2	63794	C	T	Exon3	Missense	1	GGG	GAG	NM_000623.1	1061
Bradykinin Receptor B2	BDKRB2	AE104s26	4	1543	CAGGAGAAC [T/C] GCCATCCAG	591	623	AL355102.2	63297	A	G	Exon3	Non-CDS	1			NM_000623.1	1558

Table IV (2 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	FLANK_SEQ (REF / ALT)	FLANK_SEQ REF (SEQ ID NO:)	FLANK_SEQ ALT (SEQ ID NO:)	REF_SEQ_ID	REF_SEQ_POS	REF_NT	ALT_NT	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	CDNA_SEQ_ID	CDNA_SEQ_POS
Bradykinin Receptor B2	BDKRB2	AE104s27	4	1826	AAGTGGGAA [C/T] GACTGGGCA	592	624	AL355102.2	62978	G	A	Exon3	Non-CDS	1			NM_000623.1	1877
Bradykinin Receptor B2	BDKRB2	AE104s28	4	2102	TGAGGCATC [A/T] TTACGCAGA	593	625	AL355102.2	62738	T	A	Exon3	Non-CDS	1			NM_000623.1	2117
Bradykinin Receptor B2	BDKRB2	AE104s29	4	2239	AGGTGCTCA [T/C] TGGCTCCCT	594	626	AL355102.2	62601	A	G	Exon3	Non-CDS	1			NM_000623.1	2254
Angiotensin Converting Enzyme 2	ACE2	AE109s1	7	55	TGAAAGAA [C/A] CACATGGCC	595	627	AC003669.1	68127	C	A	Intron14	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s2	10	37	ATCATAGAT [A/G] TAAATATAT	596	628	AC003669.1	89795	C	T	Intron12	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s3	10	290	AGTTGACAA [C/G] TTTCACACC	597	629	AC003669.1	89542	C	G	Intron13	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s4	11	282	ATTAGTAGC [C/T] TACCTGGT	598	630	AC003669.1	90164	C	T	Intron3	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s5	11	440	GAATGCTAA [T/C] ATAAAGATA	599	631	AC003669.1	90322	T	C	Intron2	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s6	15	109	AGAATAATG [C/T] TTGGCACAC	600	632	AC003669.1	64113	C	T	Intron16	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s7	15	241	ATCAGACAC [A/G] TTTTTAGGT	601	633	AC003669.1	64245	A	G	Exon16	Silent	1	AAT	AAC	AF241254.1	2173
Protease Inhibitor 4	PI4	AE110s1	2	447	GCCTGCAGA [T/G] GTCCTGTAC	602	634	L28101.1	8653	T	G	Intron1	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s2	2	528	CAAAGACTT [C/T] TATGTTGAT	603	635	L28101.1	6734	C	T	Exon2	Silent	0	TTC	TTT	NM_006215.1	699
Protease Inhibitor 4	PI4	AE110s3	3	188	GAGTTAGA [A/G] CATTAG	604	636	L28101.1	7821	T	C	Intron2	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s4	3	269	CCCACAAAC [T/A] GCTTCGG	605	637	L28101.1	7720	T	A	Intron2	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s5	4	563	CTTGAGCTC [A/G] CTGACCAAATC	606	638	L28101.1	3797	T	C	Exon1	Silent	0	AGT	AGC	NM_006215.1	597
Protease Inhibitor 4	PI4	AE110s6	4	1626	GAGGATGGC [T/A] ATCCTCAGA	607	639	L28101.1	2732	A	T	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s7	4	1665	TCCACAAC [A/C] TCTGTGGAG	608	640	L28101.1	2695	T	G	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s8	4	1816	CCAAAGTTG [T/C] GGGGATAG	609	641	L28101.1	2544	A	G	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s9	4	2020	TGTTTGTTT [G/C] GTTGTTTGT	610	642	L28101.1	2340	C	G	5'Flank	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	6	383	GAGCCGGGT[A/G]AGGTCTGGT	858	884	AL023653.1	69644	C	T	Intron11	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s25	13	83	GCTAGGGGC[T/C]TCGGACCTT	859	885	AL023653.1	70698	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s26	13	161	AACAGGATG[T/C]CCCAACAGG	860	886	AL023653.1	70620	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s27	18	112	TCCAGGAAC[T/C]GAGTGCCAA	861	887	AL023653.1	85621	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s28	21	261	CATGGTCCC[A/G]GGAGAGCCC	862	888	AL023653.1	84097	G	A	Exon21	Non-CDS	0			U90724.1	2689
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s29	21	293	CCTGTTGGG[C/T]ATAGCCA	863	889	AL023653.1	84129	C	T	Exon21	Non-CDS	0			U90724.1	2601
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s30	22	144	CCCTCCAGC[A/G]GGAATCTCG	864	890	AL023653.1	61848	T	C	Exon6	Silent	0	CCT	CCC	U90724.1	711
Bradykinin Receptor B1	BDKRB1	AE103s10	7	786	ACAAGGTGC[A/G]GGGGCCGCA	865	891	U48231.1	1979	G	A	Exon3	Missense	0	CGG	CAG	NM_000710.1	728
Bradykinin Receptor B1	BDKRB1	AE103s11	7	1292	GTGGGCCCT[G/A]TATAATCAC	866	892	U48231.1	2504	A	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s12	7	1806	CTCAAGGGC[T/G]CAAGTGATC	867	893	U48231.1	3025	T	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s13	7	1946	ACAAGTATC[A/G]GGTAATGGC	868	894	U48231.1	3163	G	A	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s14	7	1964	CCTCTCTTA[T/C]TACACTTCC	869	895	U48231.1	3181	T	C	Exon3	Non-CDS	0				
Bradykinin Receptor B2	BDKRB2	AE104s30	2	106	GTTGTGAGG[G/A]TTAAAGGCA	870	896	AL355102.2	62804	C	T	Exon3	Non-CDS	1			NM_000623.1	2051
Bradykinin Receptor B2	BDKRB2	AE104s31	3	93	GGCACGGAG[T/G]CCTCACGAA	871	897	AL355102.2	68030	T	G	Exon3	Missense	1	GAC	GCC	NM_000623.1	47
Bradykinin Receptor B2	BDKRB2	AE104s32	3	402	AACTGACCT[G/A]AGTACAGTG	872	898	AL355102.2	68339	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s33	3	404	CTGACCTGA[G/A]TACAGTGAA	873	899	AL355102.2	68341	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s34	6	348	TCTGCTCCA[T/C]GGAGCTATT	874	900	AL355102.2	62672	C	T	Exon3	Non-CDS	1			NM_000623.1	2183
Bradykinin Receptor B2	BDKRB2	AE104s35	6	364	ATTTCTAGA[C/A]CTCAGTGTC	875	901	AL355102.2	62688	C	A	Exon3	Non-CDS	1			NM_000623.1	2167
Bradykinin Receptor B2	BDKRB2	AE104s36	6	619	GACCGTCTC[G/A]TCGAACAGC	876	902	AL355102.2	62943	G	A	Exon3	Non-CDS	1			NM_000623.1	1912
Protease Inhibitor 4	PI4	AE110s10	2	397	GAAGCT[G/C]GTGGCT	877	903	L28101.1	9169	C	G	Exon4	Silent	0	ACC	ACG	NM_006215.1	1143
Protease Inhibitor 4	PI4	AE110s11	4	304	CACGC[A/G]TGTTTCC	878	904	L28101.1	3612	C	T	Exon1	Missense	0	CGC	TGC	NM_006215.1	412
Protease Inhibitor 4	PI4	AE110s12	4	1392	GGTACCCG[G/A]TTTCATAA	879	905	L28101.1	2524	C	T	5' Flank	Non-CDS	0				
Tachykinin Receptor 1	TACR1	AE106s8	2	92	ATGTAGAT[A/G]GTCTTGTGG	880	906	AC007400.3	141073	G	A	Intron4	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s9	3	405	CCAGA[T/G]GCAGCTAG	881	907	AC007400.3	143395	C	A	Intron3	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s8	12	359	CTTGTG[A/C]ACAGCT	882	908	AC003669.1	69475	G	T	Intron13	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s9	20	123	AAGTACA[T/C]GAAGAATT	883	909	AC003669.1	85668	C	T	Intron6	Non-CDS	1				

Table V (1 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	REFSEQ_FLANK ORIENT	REFSEQ_FLANK	REFSEQ_FLANK REF (SEQ ID NO:)	REFSEQ ALT (SEQ ID NO:)	REF_SEQ_ID	REF_SEQ_POS	REF_NT	ALT_NT	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	CDNA_SEQ_ID	CDNA_SEQ_POS
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	1	127	0	GATGTCAGCCTGCTGTCTCC[C/G]GAGCATGTGAGTGCCCCTCA	163	226	AL023653.1	82898	C	G	Exon20	Silent	0	CCC	CCG	U90724.1	2085
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	4	535	N/A	GTCTCCTTTGCAGAACAGTC[C/T]AGTGTTACACTGAGTCCAGT	164	227	AL023653.1	80150	C	T	Intron3	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s3	5	224	N/A	CCAGATTTCCCCTCACCACCT/C]TCCCCCAAGGGGGCACCCAA	165	228	AL023653.1	74483	T	C	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s4	5	392	1	GGCCACTGACAAGGCCTCAGIC/T]CCAAGCTGAGCCTCATCCTA	166	229	AL023653.1	74651	C	T	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s5	6	432	1	AGAAAGGTTGGAGTGAGGG[T/C]TGGGGCCGAGTCTCTTTTT	167	230	AL023653.1	54549	T	C	Intron1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s6	7	258	1	AGCACTCCCCAGGCCACCCC[C/T]CTTTTATTATACGCTCTATG	168	231	AL023653.1	78521	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	10	461	N/A	TTTGTTTGAGGAAAGGGTTT[C/T]GCTGCTTTTTAAGAGGATGC	169	232	AL023653.1	85586	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	13	273	1	CCTGCCAGTCCTCTGAAAAC[A/G]CCCCTGTGCCATGGAGACCT	170	233	AL023653.1	88286	A	G	Intron10	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	13	324	1	TAGAGAGCATTGCCACGAAAT/C]GGTGGCAAATCTCACGTCTG	171	234	AL023653.1	88236	T	C	Intron10	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	14	856	0	TTGCAAACGTTAGCATGCAGC/G]TGAGTCACCTGGGATGCTTG	172	235	AL023653.1	83068	C	G	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	15	187	N/A	GAAGCCCAGGCCCCAGAGGT/C]TCTCCCACCAAGGCCTCCCAC	173	236	AL023653.1	71620	C	T	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	15	194	0	AGCCCCCAGAGGTCCTCCCA[C/T]CAAGGCCTCCCACGTGACCC	174	237	AL023653.1	71627	C	T	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	15	218	0	GGCCTCCCACGTGACCCAG[T/G]ACAGGGTTAGGCTGCCCTTCT	175	238	AL023653.1	71651	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	8	221	N/A	GGAAAGGCCTGAAGGAAGAG[G/C]CCGGGGAAAGAGCCCTCCCT	176	239	AL023653.1	54356	G	C	Exon1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	8	243	1	ACCCTCTGTCTGCTCGAGCC[C/T]AGGAAAGGCCTGAAGGAAGA	177	240	AL023653.1	54334	C	T	Exon1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s16	14	139	1	CTTGCCTCAGGCAGATCAGC/A/G]TTAAATATTCCTTGTCAATT	178	241	AL023653.1	86924	A	G	Intron8	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s17	22	809	1	ACTGATACCATGTTTATGTCT/G]TCCTTTCTAGGGCCAGTGGG	179	242	AL023653.1	77205	T	G	Intron17	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s18	22	964	1	AAATAAATAATAAAAGCCAG[A/C]GCCAATCTGGTGTGTGCCAG	180	243	AL023653.1	77052	A	C	Intron17	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s19	26	195	1	CTCCTCTGGCTCCTCCTCCC[G/A]TCCTCCATATCACCTCTTCC	181	244	AL023653.1	75589	G	A	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s20	27	306	0	ACCTCTTGGCAGCTTGGCTT[A/G]GAGAGGCTGTCACCCCTTCT	182	245	AL023653.1	83469	A	G	Intron20	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s21	27	695	N/A	CCTATGGAGAAGGTCCCAGG[C/A]CCCAGGAACACAGGGCTTCT	183	246	AL023653.1	83858	C	A	Exon21	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	28	710	0	CCGGGGTTGTATACCACACC[C/G]TTGGGCCCCTAATCCCAGGCC	184	247	AL023653.1	83926	C	G	Exon21	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	28	1369	0	CAGATGAGCCAGCATTCCAG[C/T]TCTTTCACCCTTCAGCAACA	185	248	AL023653.1	84585	C	T	Exon21	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s1	6	307	0	AATTTATGTCTTTGTGGGCC[G/A]GCTCTTCAGGACCAAGGTCT	186	249	U48231.1	2207	G	A	Exon2	Missense	0	CGG	CAG	NM_000710.1	956
Bradykinin Receptor B1	BDKRB1	AE103s2	4	273	1	CTGCTGCACAGAGTGCTGCC[G/A]ACATTTATCATCTCCATCTG	187	250	U48231.1	1380	G	A	Exon2	Silent	0	CCG	CCA	NM_000710.1	129
Bradykinin Receptor B1	BDKRB1	AE103s3	7	958	1	AGAAGCTTGGCTTTCTTATC[A/G]ATTCTTTGTGACATAATAAA	188	251	U48231.1	2355	A	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s4	1	196	1	TGTTGTTGTTGAGACAGGGT[C/T]TCAGTCCGTCGGCCCAGACT	189	252	U48231.1	230	C	T	Exon1	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s5	7	240	1	ATAGTGCTAGGATTATAGGC[T/A]ATGACCACTGCCCTGGCCCC	190	253	U48231.1	3072	G	A	Exon3	Non-CDS	0				
Bradykinin Receptor B2	BDKRB2	AE104s1	10	86	N/A	CAAATCTGCAGGGCTCCCCC[C/G]CCCTCGCCCAGGTGGGCCCC	191	254	AL355102.2	98426	C	G	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s2	10	87	0	AAATCTGCAGGGCTCCCCCC[A/G]CCGCGCCCAGGTGGGCCCCT	192	255	AL355102.2	98427	A	G	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s3	10	462	0	AAGGGCTGGCTGAGGTCATG[T/A]TCCCGCTCTGAGACTCAGTT	193	256	AL355102.2	98802	T	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s4	10	542	0	CAGGGAGAGCTGGGATGAGG[C/T]CTGGGGTGCTGCCTGTGGGG	194	257	AL355102.2	98882	C	T	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s5	10	557	0	TGAGGCCTGGGGTGCTGCC[T/G/A]TGGGGACAGCACGCATGCTT	195	258	AL355102.2	98897	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s6	10	717	N/A	TGCTGCCAGGGCCCGAAGAG[G/A]CAGCACAGTTTTTCTCCAG	196	259	AL355102.2	99056	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s7	7	408	1	GCCCTGGAGGGAGCAGGGGG[G/C]TTGTGGGACACAGACTTGGA	197	260	AL355102.2	86389	G	C	Intron2	Non-CDS	1			NM_000623.1	2002
Bradykinin Receptor B2	BDKRB2	AE104s8	5	275	1	GGGAACTGAGGCAGGGACAG[A/G]TGGTTGTGCAATAGTTATTG	198	261	AL355102.2	82853	A	G	Exon3	Non-CDS	1			NM_000623.1	2117
Bradykinin Receptor B2	BDKRB2	AE104s9	5	390	1	TCCCAGTTACGTCTGCGTAAT/A/G]ATGCCTCACATGTACGTAG	199	262	AL355102.2	82738	T	A	Exon3	Non-CDS	1			NM_000623.1	2254
Bradykinin Receptor B2	BDKRB2	AE104s10	5	527	1	TGACAGGTGGAAGGGAGCCA/A/G]TGAGCACCTACTGTGTGCCA	200	263	AL355102.2	82601	A	G	Exon3	Non-CDS	1			NM_000623.1	3804
Bradykinin Receptor B2	BDKRB2	AE104s11	8	579	0	ATAACAGCTCATTGAGTCTTT/G]CACAGGACAGATGTTCTTTA	201	264	AL355102.2	81132	T	G	Exon3	Non-CDS	1			NM_000623.1	3598
Bradykinin Receptor B2	BDKRB2	AE104s12	8	585	0	GCTCATTGAGTCTTTCACAG[G/T]ACAGATGTTCTTTATCAGGG	202	265	AL355102.2	81138	G	T	Exon3	Non-CDS	1			NM_000623.1	3456
Bradykinin Receptor B2	BDKRB2	AE104s13	6	727	N/A	AAGAGAGTCTCAGACCATCA[C/T]GTGCTCTGGTGCTGAATGAC	203	266	AL355102.2	61260	C	T	Exon3	Non-CDS	1			NM_000623.1	2585
Bradykinin Receptor B2	BDKRB2	AE104s14	8	482	N/A	GCCGATGGTGAACACCATTG[C/T]CATTCCTTTTCACACTCTTC	204	267	AL355102.2	62200	C	T	Exon3	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s15	9	1010	1	TATGGAGACAGACTAGGCAAI[G/A]TTTTGTTTAATAAATGAGTG	205	268	AL355102.2	60403	G	A	3' Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s16	9	1072	1	TGAGCGATGAGCCCCAGGTTC/T]CTGGCATGGATGGATGGATG	206	269	AL355102.2	60341	C	T	3' Flank	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s1	1	614	1	GCGAAGACAGCGGCGATGGG[A/G]AAGAAGTTGTGGAACTTGCA	207	270	AC007681.3	103665	A	G	Exon1	Silent	1	TTT	TTC	NM_001058.2	543
Tachykinin Receptor 1	TACR1	AE106s2	2	789	N/A	AGCAGGAGAGCCAGGACCCA[G/T]ATGACACAGATGACCACTTT	208	271	AC007681.3	25759	G	T	Exon2	Silent	1	ATC	ATA	NM_001058.2	672
Tachykinin Receptor 1	TACR1	AE106s3	4	676	0	GGGTGGGTTAGTTCTGCCTG[T/G]CCCCTGCTCACCTTGCGCTT	209	272	AC007400.3	143458	T	G	Intron5	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s4	8	152	0	CAGAATGGAATGAATGGGCTTT/C]TTGGAAAAGCTGGTCCGAC	210	273	AC007400.3	139028	T	C	Exon5	Non-CDS	1			NM_001058.2	1835
Tachykinin Receptor 1	TACR1	AE106s5	8	220	0	CAGTGATTTGGTTTGAGTCAC/A]ACAGCATGAGGGTGGCAAAG	211	274	AC007400.3	139096	C	A	Exon5	Non-CDS	1			NM_001058.2	1538
Tachykinin Receptor 1	TACR1	AE106s6	6	317	N/A	CTGACCCTTTTTGCAAGTCC[C/T]AGTGTGAGGGTGTTTCTGAT	212	275	AC007400.3	139193	C	T	Exon5	Silent	1	TCG	TCA	NM_001058.2	1344
Tachykinin Receptor 1	TACR1	AE106s7	6	511	0	TTGGAGGTCAGGTCCAGGGA[C/T]GAGGGTGTGGCCTTGGGGCC	213	276	AC007400.3	139387	C	T	Exon5	Silent	1	TCG	TCA	NM_001058.2	1344
C1 Esterase Inhibitor	C1NH	AE105s1	3	319	0	CGCTGGGGAAAGAAAGGACA[G/A]AGGGAATGTTGGAGCTACAG	214	277	X54486.1	5755	G	A	Intron4	Non-CDS	0				
C1 Esterase Inhibitor	C1NH	AE105s2	5	158	0	GCAGTAGGAAGACTGTTAA[A/G]TGCATCTCTTATTTTCTAGG	215	278	X54486.1	15193	A	G	Intron6	Non-CDS	0				
C1 Esterase Inhibitor	C1NH	AE105s3	5	366	0	CGCATCAAAGTGACGACCAG[C/T]CAGGATATGCTCTCAATCAT	216	279	X54486.1	15401	C	T	Exon7	Silent	0	AGC	AGT	NM_000062.1	1278
C1 Esterase Inhibitor	C1NH	AE105s4	7	588	0	TATCTCCAAGATGCTATTCGT/C]TGAACCCATGCTGGAGGTTT	217	280	X54486.1	3493	T	C	Exon3	Missense	0	GTT	GCT	NM_000062.1	227
C1 Esterase Inhibitor	C1NH	AE105s5	7	897	0	GCTCTACCACGCCTTCTCAG[C/G]AATGAAGAAGGTGGAGACCA	218	281	X54486.1	3802	C	G	Exon3	Missense	0	GCA	GGA	NM_000062.1	536
C1 Esterase Inhibitor	C1NH	AE105s6	8	276	N/A	TGCAGCAGCCCTTCCTCTTG[G/A]TGCTCTGGAACCAGCAGCAC	219	282	X54486.1	18012	G	A	Exon8	Missense	0	GTG	ATG	NM_000062.1	1496
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	1	153	1	TCCTGCCTAATGATGAGTGC/A/G]AAAAGCCCACGTCCAGAAG	220	283	AF277050.1	4773	A	G	Exon4	Missense	0	AAA	GAA	NM_002257.1	592
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	1	299	1	CAGACTGTGTAGCCCAAGGC[G/A]GGGATGGGGACTCCTGCGTC	221	284	AF277050.1	4627	G	A	Intron3	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	2	805	0	AGGTCGTGGAGTTGCCCACG[G/C]AGGAACCCGAAGTGGGGAGC	222	285	AF277050.1	4533	G	C	Exon3	Missense	0	GAG	CAG	NM_002257.1	469
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s4	2	717	0	GGCGGGGATGGGGACTCCTG[C/T]GTCCAAGGGAGAAAGGGCCA	223	286	AF277050.1	4644	C	T	Intron3	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s5	4	632	1	GGGCCACCCCAGCTGTGTCA[A/G]TCTCATGCCTGGAAGTCTGA	224	287	AF277050.1	5593	A	G	3' Flank	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s6	4	897	1	TGTCACGTTCTGCCATCACC[T/C]ATCTTTCCAGATGTGGTGCA	225	288	AF277050.1	5678	T	C	3' Flank	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s6	1	67	N/A	CTCCTCTGCCGTGTCATCAA[C/T]GGGGTCATCAAGGCCAATTT	643	675	U48231.1	1599	C	T	Exon0	Silent	0	AAC	AAT	NM_000710.1	348
Bradykinin Receptor B1	BDKRB1	AE103s7	1	181	0	GGAAGGCAGCAGCGGCGGAG[G/A]CAGCGCCGGGTCACCTGCGT	644	676	U48231.1	1713	G	A	Exon0	Silent	0	AGG	AGA	NM_000710.1	462
Bradykinin Receptor B1	BDKRB1	AE103s8	1	298	0	TGAACATCACCGCCTGCATC[C/G]TGCTCCTCCCCCATGAGGCC	645	677	U48231.1	1828	C	G	Exon0	Missense	0	CTG	GTG	NM_000710.1	577

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GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	REFSEQ_FLANK ORIENT	REFSEQ_FLANK	REFSEQ_FLANK REF (SEQ ID NO:)	REFSEQ ALT (SEQ ID NO:)	REF_SEQ_ID	REF_SEQ_POS	REF_NT	ALT_NT	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	CDNA_SEQ_ID	CDNA_SEQ_POS
Bradykinin Receptor B1	BDKRB1	AE103s9	2	136	0	GCCTCCCTGCGAACGCGGGA(G/A)AGGTCAGCAGGACAAGAGT	646	678	U48231.1	1958	G	A	Exon3	Silent	0	GAG	GAA	NM_000710.1	705
Bradykinin Receptor B2	BDKRB2	AE104s18	7	202	1	CTGGGGATTGCAAAATACAC(G/T)CATTCTCCAGCAGGGAGGAG	647	679	AL355102.2	88174	G	T	Intron1 or Exon2	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s19	7	330	1	GGTGGGCACGGAGTCCTCAC(G/A)AACAGACAGAAACATTGATA	648	680	AL355102.2	89037	G	A	Exon2	Missense	1	CGT	TGT	NM_000623.1	40
Bradykinin Receptor B2	BDKRB2	AE104s20	2	271	N/A	AGCCTTAAAACCCTTCCTTC(A/C)AAGAGAACAGATAAGAGTG	649	681	AL355102.2	101078	A	C	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s21	3	406	1	AGCTGTCCTGTTTCCTGGGT(A/G)CGGGTGTTTGCGCTCCCCTG	650	682	AL355102.2	100859	A	G	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s22	3	463	1	AGTCCTGGGATTTCTTTGTAT(T/C)GCCACGTACGGCTCCCAAGG	651	683	AL355102.2	100804	T	C	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s23	3	886	1	CATCTTTCAAGGGATGGGTA(G/A)TGATGTCATCAGCCTCCTGG	652	684	AL355102.2	100381	G	A	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s24	4	918	1	GAGGCGATCTGTGTGATTAC(A/G)TCGATGATGCGCTCGTCCTG	653	685	AL355102.2	63922	A	G	Exon3	Silent	1	GAT	GAC	NM_000623.1	933
Bradykinin Receptor B2	BDKRB2	AE104s25	4	1046	1	TGGGTTCTGACCTGCAGCCCG(C/T)CTTTCTGGCACACTCCCTGG	654	686	AL355102.2	63794	C	T	Exon3	Missense	1	GGG	GAG	NM_000623.1	1061
Bradykinin Receptor B2	BDKRB2	AE104s26	4	1543	1	TTGCACCAAAGCTGGATGGC(A/G)GTTCTCCTGGAGATCTAAGT	655	687	AL355102.2	63297	A	G	Exon3	Non-CDS	1			NM_000623.1	1558
Bradykinin Receptor B2	BDKRB2	AE104s27	4	1826	1	GGTGGTGGCAGTGCCCAGTC(G/A)TTCCCACTTGAGTCTTTGAG	656	688	AL355102.2	62978	G	A	Exon3	Non-CDS	1			NM_000623.1	1977
Bradykinin Receptor B2	BDKRB2	AE104s28	4	2102	1	TCCCAGTTACGTCTGCGTAA(T/A)GATGCCTCACATGTACGTAG	657	689	AL355102.2	62738	T	A	Exon3	Non-CDS	1			NM_000623.1	2117
Bradykinin Receptor B2	BDKRB2	AE104s29	4	2239	1	TGACAGGTGGAAGGGAGCCA(A/G)TGAGCACCTACTGTGTGCCA	658	690	AL355102.2	62601	A	G	Exon3	Non-CDS	1			NM_000623.1	2254
Angiotensin Converting Enzyme 2	ACE2	AE109s1	7	55	0	ACTTATAGTTTTGAAAAGAA(C/A)CACATGAGCCTCTCTTCTTTC	659	691	AC003669.1	68127	C	A	Intron14	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s2	10	37	1	TCCAGATGTACATATATTTA(C/T)ATCTATGATCTATGGTTTCT	660	692	AC003669.1	69795	C	T	Intron12	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s3	10	290	1	GACAAGGAATGGGTGTGAAA(C/G)TTGTCAACTGGGTGTACTCA	661	693	AC003669.1	69542	C	G	Intron13	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s4	11	282	0	CACTACTAAAAATTAGTAGC(C/T)TACCTGGTTCAAGTAATAAG	662	694	AC003669.1	90184	C	T	Intron3	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s5	11	440	0	TTTGCTGAAGAGAATGCTAAT(T/C)ATAAAGATATCCTTTGACC	663	695	AC003669.1	90322	T	C	Intron2	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s6	15	109	0	GTAAATGACTCAGAATAATG(C/T)TTGGCACACAGGAAGAACAC	664	696	AC003669.1	84113	C	T	Intron18	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s7	15	241	0	CTAGGAATGATATCAGACAC(A/G)TTTTTAGGTGCAGTGACAAA	665	697	AC003669.1	84245	A	G	Exon18	Silent	1	AAT	AAC	AF241254.1	2173
Protease Inhibitor 4	PI4	AE110s1	2	447	0	CTAGCTCTGTGGCCTGCAGA(T/G)GTCCTGTACCTTCTTTTCAT	666	698	L28101.1	8653	T	G	Intron1	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s2	2	526	0	AGGACCACTCCCAAAGACTTTC(T/TATGTTGATGAGAACACAAC	667	699	L28101.1	6734	C	T	Exon2	Silent	0	TTC	TTT	NM_006215.1	899
Protease Inhibitor 4	PI4	AE110s3	3	168	1	GCTTGTTCATTAATCTAATGT(T/C)TCAACTCAATGCCCCTTTC	668	700	L28101.1	7821	T	C	Intron2	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s4	3	269	1	GAGGTGGTCTGAGCCGAAGGT(A/G)TTTGTGGGGACAGAACTCA	669	701	L28101.1	7720	T	A	Intron2	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s5	4	563	1	AAGATTGTGGATTTGGTCAG(T/C)GAGCTCAAGAAGGACGTCTT	670	702	L28101.1	3797	T	C	Exon1	Silent	0	AGT	AGC	NM_006215.1	597
Protease Inhibitor 4	PI4	AE110s6	4	1628	1	CTAAAATAAACTCTGAGGAT(A/T)GCCATCCTCCATGCAAAATC	671	703	L28101.1	2732	A	T	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s7	4	1865	1	CATATAAAGCACTCCACAGA(T/G)GTTTGTGGAACAGACCCTAA	672	704	L28101.1	2695	T	G	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s8	4	1818	1	CGGGTACCAATTCTATCCCG(A/G)CAACTTTGGGCAGGTCACTT	673	705	L28101.1	2544	A	G	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s9	4	2020 -	1	CAAACAAACAAACAAACAAC(C/G)AAACAAACAAAAAAAACCCA	674	706	L28101.1	2340	C	G	5'Flank	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	6	383	1	CTGTGGCTGCAACCAGACGT(C/T)ACCCGGCTCCTCTGTTTCCC	910	936	AL023653.1	89644	C	T	Intron11	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s25	13	83	1	AGTCCACGTTGAAGGTCCGA(G/A)GCCCCTAGCCCTGTGGGGGC	911	937	AL023653.1	70698	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s26	13	161	1	TTTTCTAGGGCCCTGTTGGG(G/A)CATCCTGTTGTGTGTAGA	912	938	AL023653.1	70620	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s27	18	112	0	AAGGCTGACCTTCCAGGAAG(C/T)GAGTGCCAAAGGCAAGGTCT	913	939	AL023653.1	85421	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s28	21	261	0	CCCAAGGGTGCCATGGTCCC(G/A)GGAGAGCCCAAACCTATCAC	914	940	AL023653.1	84097	G	A	Exon21	Non-CDS	0			U90724.1	2680
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s29	21	293	0	ACCTATCACCACCTGTTGGG(C/T)ATAGCCAGAGCTGTTCCCAC	915	941	AL023653.1	84129	C	T	Exon21	Non-CDS	0			U90724.1	2901
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s30	22	144	1	TGGGTCCTCACCGAGATTCGT(C/G)CTGGAGGGCGTGTGGGTTT	916	942	AL023653.1	81848	T	C	Exon6	Silent	0	CCT	CCC	U90724.1	711
Bradykinin Receptor B1	BDKRB1	AE103s10	7	766	0	GGTCAGCAGGACAAGAGTGC(G/A)GGGGCCGAAGGATAGCAAGA	917	943	U48231.1	1979	G	A	Exon3	Missense	0	CGG	CAG	NM_000710.1	729
Bradykinin Receptor B1	BDKRB1	AE103s11	7	1292	0	GAATTATCCAAGTGGGCCCT(A/G)TATAATCACAAGGGTCCTTA	918	944	U48231.1	2504	A	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s12	7	1808	0	CTGGTCTCAAACTCAAGGGCT(C/G)CAAGTGATCCTCCACTTTGG	919	945	U48231.1	3025	T	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s13	7	1946	0	GGAAACAAATAACAAGTATC(G/A)GGTAATGGCCTCTCTTATTA	920	946	U48231.1	3163	G	A	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s14	7	1964	0	TCGGGTAATGGGCTCTCTTATA(T/C)TAGACTTCCATTTGTCTATT	921	947	U48231.1	3181	T	C	Exon3	Non-CDS	0				
Bradykinin Receptor B2	BDKRB2	AE104s30	2	108	1	ATACCTGTTACTGCCTTTAA(C/T)CCTCACAACGACTTCATGTT	922	948	AL355102.2	62804	C	T	Exon3	Non-CDS	1			NM_000623.1	2051
Bradykinin Receptor B2	BDKRB2	AE104s31	3	93	0	AGGCCGTGGTGGGCACGGAG(T/A)CCTCACGAACAGACAGAAAC	923	949	AL355102.2	68030	T	G	Exon3	Missense	1	GAC	GCC	NM_000623.1	47
Bradykinin Receptor B2	BDKRB2	AE104s32	3	402	0	TAATAACTGCAAACTGACCT(G/A)AGTACAGTGAAAAATCAAGC	924	950	AL355102.2	68339	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s33	3	404	0	ATAACTGCAAACTGACCTGA(G/A)TACAGTGAAAAATCAAGCAA	925	951	AL355102.2	68341	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s34	6	348	0	CCAATACTGATTCTGCTCCA(C/T)GGAGCTATTTCTAGACCTCA	926	952	AL355102.2	62672	C	T	Exon3	Non-CDS	1			NM_000623.1	2183
Bradykinin Receptor B2	BDKRB2	AE104s35	6	364	0	TCGACGGAGCTATTTCTAGA(C/A)CTCAGTGTCTTTTCCTTATA	927	953	AL355102.2	62686	C	A	Exon3	Non-CDS	1			NM_000623.1	2167
Bradykinin Receptor B2	BDKRB2	AE104s36	6	819	0	GCACCCTGCTCGACCGTCTC(G/A)TCGAACAGCTTTCTGGTGGT	928	954	AL355102.2	62043	G	A	Exon3	Non-CDS	1			NM_000623.1	1912
Protease Inhibitor 4	PI4	AE110s10	2	397	1	ACCGAAGGCTGCAGCAGCCAC(C/G)ACGTTCGCGATCAAATTCTT	929	955	L28101.1	9180	C	G	Exon4	Silent	0	ACC	ACG	NM_006215.1	1143
Protease Inhibitor 4	PI4	AE110s11	4	304	1	CCGGCCATGGGCTGGAAACA(C/T)GCGTGGGCAGTGCTCTGTTC	930	956	L28101.1	3612	C	T	Exon1	Missense	0	CGC	TGC	NM_006215.1	412
Protease Inhibitor 4	PI4	AE110s12	4	1392	1	GACAGATGTTCATTATGAAA(C/T)GGGTACCAATTCTATCCCCA	931	957	L28101.1	2524	C	T	5' Flank	Non-CDS	0				
Tachykinin Receptor 1	TACR1	AE106s8	2	92	0	TGGCCACTGTGTATGTAGAT(G/A)GTCTTGTGGCCCCTGGAGAG	932	958	AC007400.3	141073	G	A	Intron4	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s9	3	405	1	GGATATTTTGTGCTAGCTGC(C/A)TCTGGGGCTCACAAGTGTGC	933	959	AC007400.3	143385	C	A	Intron3	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s8	12	359	1	AAAGAAACATTCTCAGCTGTG(T/C)TCACAAGTCCTCATGAGACT	934	960	AC003669.1	69475	G	T	Intron13	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s9	20	123	0	ATAACAAAGAGCCAAGTACA(C/T)GAAGAATTCATGGGGCTTCT	935	961	AC003669.1	85668	C	T	Intron6	Non-CDS	1				
Kallikrein 1 (renal/pancreas/saliva/r)	KLK1	AE107s2	1	299	0	GACGCAGGAGTCCCCATCC (C/T) CGCCTTGGGCTACACAGTCTG	1574	1575	AF277050.1	4627	G	A	Intron3	Non-CDS	N/A				

Table VI

GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	REF_AA	ALT_AA	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	PROTEIN_ID	PROTEIN_POS	PROTEIN (SEQ ID NO:)	FLANK_SEQ REF (SEQ ID NO:)	FLANK_SEQ ALT (SEQ ID NO:)	REFSEQ_FLANK REF (SEQ ID NO:)
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	1	127	P	P	Exon20	Silent	0	CCC	CCG	AAB96394.1	607	4	37	100	163
Bradykinin Receptor B1	BDKRB1	AE103s1	6	307	R	Q	Exon2	Missense	0	CGG	CAG	NP_000701.1	317	6	60	123	186
Bradykinin Receptor B1	BDKRB1	AE103s2	4	273	P	P	Exon2	Silent	0	CCG	CCA	NP_000701.1	41	10	61	124	187
Tachykinin Receptor 1	TACR1	AE106s1	1	614	F	F	Exon1	Silent	1	TTT	TTC	NP_001049.1	111	18	81	144	207
Tachykinin Receptor 1	TACR1	AE106s2	2	789	I	I	Exon2	Silent	1	ATC	ATA	NP_001049.1	154	18	82	145	208
Tachykinin Receptor 1	TACR1	AE106s7	6	511	S	S	Exon5	Silent	1	TCG	TCA	NP_001049.1	378	20	87	150	213
C1 Esterase Inhibitor	C1NH	AE105s3	5	366	S	S	Exon7	Silent	0	AGC	AGT	NP_000053.1	406	24	90	153	216
C1 Esterase Inhibitor	C1NH	AE105s4	7	588	V	A	Exon3	Missense	0	GTT	GCT	NP_000053.1	56	26	91	154	217
C1 Esterase Inhibitor	C1NH	AE105s5	7	897	A	G	Exon3	Missense	0	GCA	GGA	NP_000053.1	159	26	92	155	218
C1 Esterase Inhibitor	C1NH	AE105s6	8	276	V	M	Exon8	Missense	0	GTG	ATG	NP_000053.1	480	30	93	156	219
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	1	153	K	E	Exon4	Missense	0	AAA	GAA	NP_002248.1	186	34	94	157	220
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	2	605	E	Q	Exon3	Missense	0	GAG	CAG	NP_002248.1	145	36	96	159	222
Bradykinin Receptor B1	BDKRB1	AE103s6	1	67	N	N	Exon3	Silent	0	AAC	AAT	NP_000701.1	114	556	579	611	643
Bradykinin Receptor B1	BDKRB1	AE103s7	1	181	R	R	Exon3	Silent	0	AGG	AGA	NP_000701.1	152	558	580	612	644
Bradykinin Receptor B1	BDKRB1	AE103s8	1	296	L	V	Exon3	Missense	0	CTG	GTG	NP_000701.1	191	560	581	613	645
Bradykinin Receptor B1	BDKRB1	AE103s9	2	136	E	E	Exon3	Silent	0	GAG	GAA	NP_000701.1	233	562	582	614	646
Bradykinin Receptor B2	BDKRB2	AE104s19	7	339	R	C	Exon2	Missense	1	CGT	TGT	NP_000614.1	14	564	584	616	648
Bradykinin Receptor B2	BDKRB2	AE104s24	4	916	D	D	Exon3	Silent	1	GAT	GAC	NP_000614.1	311	566	589	621	653
Bradykinin Receptor B2	BDKRB2	AE104s25	4	1046	G	E	Exon3	Missense	1	GGG	GAG	NP_000614.1	354	568	590	622	654
Angiotensin Converting Enzyme 2	ACE2	AE109s7	15	241	N	N	Exon16	Silent	1	AAT	AAC	AAF78220.1	690	843	601	633	665
Protease Inhibitor 4	PI4	AE110s2	2	528	F	F	Exon2	Silent	0	TTC	TTT	NP_006206.1	233	574	603	635	667
Protease Inhibitor 4	PI4	AE110s5	4	563	S	S	Exon1	Silent	0	AGT	AGC	NP_006206.1	199	576	606	638	670

Table VIIA

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
Coriell 24 panel	NA14905	African American	x	x	x	x	x			
Coriell 24 panel	NA14922	African American	x	x	x	x	x			
Coriell 24 panel	NA14923	African American	x	x	x	x	x			
Coriell 24 panel	NA14924	African American	x	x	x	x	x			
Coriell 24 panel	NA14925	African American	x	x	x	x	x			
Coriell 24 panel	NA14932	African American	x	x	x	x	x			
Coriell 24 panel	NA14933	African American	x	x	x	x	x			
Coriell 24 panel	NA14934	African American	x	x	x	x	x			
Coriell 24 panel	NA 17201	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17202	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17203	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17204	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17205	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17206	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17207	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17208	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA00576	Chinese	x	x	x	x	x			
Coriell 24 panel	NA03433	Chinese	x	x	x	x	x			
Coriell 24 panel	NA06090	Chinese	x	x	x	x	x			
Coriell 24 panel	NA07426	Chinese	x	x	x	x	x			
Coriell 24 panel	NA02345b	Japanese	x	x	x	x	x			
Coriell 24 panel	NA11589	Japanese	x	x	x	x	x			
Coriell 24 panel	NA14819	Japanese	x	x	x	x	x			
Coriell 24 panel	NA04535	Japanese	x	x	x	x	x			
Coreill 8 panel	NA14672	African American						x	x	x
Coreill 8 panel	NA14682	African American						x	x	x
Coreill 8 panel	NA14683	African American						x	x	x
Coreill 8 panel	NA14696	African American						x	x	x
Coreill 8 panel	NA14698	African American						x	x	x
Coreill 8 panel	NA14700	African American						x	x	x
Coreill 8 panel	NA14704	African American						x	x	x
HD 50 AA panel	NA1850	African American	x							
HD 50 AA panel	3382	African American	x							
HD 50 AA panel	3725	African American	x							
HD 50 AA panel	6865	African American	x							
HD 50 AA panel	7754	African American	x							
HD 50 AA panel	10251	African American	x							
HD 50 AA panel	10378	African American	x							
HD 50 AA panel	12931	African American	x							
HD 50 AA panel	13294	African American	x							
HD 50 AA panel	14439	African American	x							
HD 50 AA panel	14441	African American	x							
HD 50 AA panel	14454	African American	x							
HD 50 AA panel	14464	African American	x							

Table VIIB

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 50 AA panel	14537	African American	x							
HD 50 AA panel	14583	African American	x							
HD 50 AA panel	14681	African American	x							
HD 50 AA panel	14687	African American	x							
HD 50 AA panel	14697	African American	x							
HD 50 AA panel	14699	African American	x							
HD 50 AA panel	14720	African American	x							
HD 50 AA panel	14746	African American	x							
HD 50 AA panel	14754	African American	x							
HD 50 AA panel	14755	African American	x							
HD 50 AA panel	14771	African American	x							
HD 50 AA panel	14772	African American	x							
HD 50 AA panel	14783	African American	x							
HD 50 AA panel	14826	African American	x							
HD 50 AA panel	14837	African American	x							
HD 50 AA panel	14862	African American	x							
HD 50 AA panel	14863	African American	x							
HD 50 AA panel	14864	African American	x							
HD 50 AA panel	14892	African American	x							
HD 50 AA panel	14893	African American	x							
HD 50 AA panel	14894	African American	x							
HD 50 AA panel	14895	African American	x							
HD 50 AA panel	14897	African American	x							
HD 50 AA panel	14900	African American	x							
HD 50 AA panel	14901	African American	x							
HD 50 AA panel	14903	African American	x							
HD 50 AA panel	14904	African American	x							
HD 50 AA panel	14905	African American	x							
HD 50 AA panel	14922	African American	x							
HD 50 AA panel	14923	African American	x							
HD 50 AA panel	14924	African American	x							
HD 50 AA panel	14925	African American	x							
HD 50 AA panel	14932	African American	x							
HD 50 AA panel	14933	African American	x							
HD 100 CAU panel	NA 17201	Caucasian		x						
HD 100 CAU panel	17202	Caucasian		x						
HD 100 CAU panel	17203	Caucasian		x						
HD 100 CAU panel	17204	Caucasian		x						
HD 100 CAU panel	17205	Caucasian		x						
HD 100 CAU panel	17206	Caucasian		x						
HD 100 CAU panel	17207	Caucasian		x						
HD 100 CAU panel	17208	Caucasian		x						
HD 100 CAU panel	17209	Caucasian		x						
HD 100 CAU panel	17210	Caucasian		x						

Table VIIC

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17211	Caucasian		x						
HD 100 CAU panel	17212	Caucasian		x						
HD 100 CAU panel	17213	Caucasian		x						
HD 100 CAU panel	17214	Caucasian		x						
HD 100 CAU panel	17215	Caucasian		x						
HD 100 CAU panel	17216	Caucasian		x						
HD 100 CAU panel	17217	Caucasian		x						
HD 100 CAU panel	17218	Caucasian		x						
HD 100 CAU panel	17219	Caucasian		x						
HD 100 CAU panel	17220	Caucasian		x						
HD 100 CAU panel	17221	Caucasian		x						
HD 100 CAU panel	17222	Caucasian		x						
HD 100 CAU panel	17223	Caucasian		x						
HD 100 CAU panel	17224	Caucasian		x						
HD 100 CAU panel	17225	Caucasian		x						
HD 100 CAU panel	17226	Caucasian		x						
HD 100 CAU panel	17227	Caucasian		x						
HD 100 CAU panel	17228	Caucasian		x						
HD 100 CAU panel	17229	Caucasian		x						
HD 100 CAU panel	17230	Caucasian		x						
HD 100 CAU panel	17231	Caucasian		x						
HD 100 CAU panel	17232	Caucasian		x						
HD 100 CAU panel	17233	Caucasian		x						
HD 100 CAU panel	17234	Caucasian		x						
HD 100 CAU panel	17235	Caucasian		x						
HD 100 CAU panel	17236	Caucasian		x						
HD 100 CAU panel	17237	Caucasian		x						
HD 100 CAU panel	17238	Caucasian		x						
HD 100 CAU panel	17239	Caucasian		x						
HD 100 CAU panel	17240	Caucasian		x						
HD 100 CAU panel	17241	Caucasian		x						
HD 100 CAU panel	17242	Caucasian		x						
HD 100 CAU panel	17243	Caucasian		x						
HD 100 CAU panel	17244	Caucasian		x						
HD 100 CAU panel	17245	Caucasian		x						
HD 100 CAU panel	17246	Caucasian		x						
HD 100 CAU panel	17247	Caucasian		x						
HD 100 CAU panel	17248	Caucasian		x						
HD 100 CAU panel	17249	Caucasian		x						
HD 100 CAU panel	17250	Caucasian		x						
HD 100 CAU panel	17251	Caucasian		x						
HD 100 CAU panel	17252	Caucasian		x						
HD 100 CAU panel	17253	Caucasian		x						
HD 100 CAU panel	17254	Caucasian		x						

Table VIID

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17255	Caucasian		x						
HD 100 CAU panel	17256	Caucasian		x						
HD 100 CAU panel	17257	Caucasian		x						
HD 100 CAU panel	17258	Caucasian		x						
HD 100 CAU panel	17259	Caucasian		x						
HD 100 CAU panel	17260	Caucasian		x						
HD 100 CAU panel	17261	Caucasian		x						
HD 100 CAU panel	17262	Caucasian		x						
HD 100 CAU panel	17263	Caucasian		x						
HD 100 CAU panel	17264	Caucasian		x						
HD 100 CAU panel	17265	Caucasian		x						
HD 100 CAU panel	17266	Caucasian		x						
HD 100 CAU panel	17267	Caucasian		x						
HD 100 CAU panel	17268	Caucasian		x						
HD 100 CAU panel	17269	Caucasian		x						
HD 100 CAU panel	17270	Caucasian		x						
HD 100 CAU panel	17271	Caucasian		x						
HD 100 CAU panel	17272	Caucasian		x						
HD 100 CAU panel	17273	Caucasian		x						
HD 100 CAU panel	17274	Caucasian		x						
HD 100 CAU panel	17275	Caucasian		x						
HD 100 CAU panel	17276	Caucasian		x						
HD 100 CAU panel	17277	Caucasian		x						
HD 100 CAU panel	17278	Caucasian		x						
HD 100 CAU panel	17279	Caucasian		x						
HD 100 CAU panel	17280	Caucasian		x						
HD 100 CAU panel	17281	Caucasian		x						
HD 100 CAU panel	17282	Caucasian		x						
HD 100 CAU panel	17283	Caucasian		x						
HD 100 CAU panel	17284	Caucasian		x						
HD 100 CAU panel	17285	Caucasian		x						
HD 100 CAU panel	17286	Caucasian		x						
HD 100 CAU panel	17287	Caucasian		x						
HD 100 CAU panel	17288	Caucasian		x						
HD 100 CAU panel	17289	Caucasian		x						
HD 100 CAU panel	17290	Caucasian		x						
HD 100 CAU panel	17291	Caucasian		x						
HD 100 CAU panel	17292	Caucasian		x						
HD 100 CAU panel	17293	Caucasian		x						
HD 100 CAU panel	17294	Caucasian		x						
HD 100 CAU panel	17295	Caucasian		x						
Omapatrilat Trial Samples	12 angioedema patients			x	x	x	x	x	x	x

Table VIII(1 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	PCR Amplicon_Name	Target_Name	PCR Left primer	PCR Left primer (SEQ ID NO:)	PCR Right primer	PCR Right primer (SEQ ID NO:)
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	Exon20	0	AE100p77p78	XPNPEP2_X20a	AGTGCTCCTTCCTTCCCTTC	297	TATTCACTACCTGGGGTTGGG	360
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	Intron3	0	AE100p9p10	XPNPEP2_X3a	CAGCCCAGGCATCTTAATCTA	298	TCTCTACTTCCCTCCCTTTGC	361
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s3	Intron15	0	AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCTTCCTTTCGC	299	ATAGGATGAGGCTCAGCTTGG	362
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s4	Intron15	0	AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCTTCCTTTCGC	300	ATAGGATGAGGCTCAGCTTGG	363
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s5	Intron1	0	AE100p1p2	XPNPEP2_X1a	TGATTGAGACCAGCTGTTGTG	301	AACAGAAAAAGAGACTCGGGC	364
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s6	Intron7	0	AE100p25p26	XPNPEP2_X7a	CCAGCGTGGGCATACATG	302	GGCCCTGAAATCTGCATTT	365
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	Intron7	0	AE100p25p26	XPNPEP2_X7a	CCAGCGTGGGCATACATG	303	GGCCCTGAAATCTGCATTT	366
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	Intron10	0	AE100p37p38	XPNPEP2_X10a	CTTCCTTTGACCTCCAGGAAC	304	CCTGTTTCCTCTTCTGGCTCT	367
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	Intron10	0	AE100p37p38	XPNPEP2_X10a	CTTCCTTTGACCTCCAGGAAC	305	CCTGTTTCCTCTTCTGGCTCT	368
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	Intron7	0	AE100p25p26	XPNPEP2_X7a	CCAGCGTGGGCATACATG	306	GGCCCTGAAATCTGCATTT	369
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	307	CAGCTCTCAGGCCTTTTCATT	370
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	308	CAGCTCTCAGGCCTTTTCATT	371
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	309	CAGCTCTCAGGCCTTTTCATT	372
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	Exon1	0	AE100p1p2	XPNPEP2_X1a	TGATTGAGACCAGCTGTTGTG	310	AACAGAAAAAGAGACTCGGGC	373
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	Exon1	0	AE100p1p2	XPNPEP2_X1a	TGATTGAGACCAGCTGTTGTG	311	AACAGAAAAAGAGACTCGGGC	374
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s16	Intron8	0	AE100p29p30	XPNPEP2_X8a	GGCCCATGTCATTAATGAGTAC	312	TCAGGGCTACCTTTTGTCCTT	375
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s17	Intron17	0	AE100p65p66	XPNPEP2_X17a	CCCTCTTCTTAGGCACCACTC	313	CTGCTGGCATTCCTCACTTAC	376
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s18	Intron17	0	AE100p65p66	XPNPEP2_X17a	CCCTCTTCTTAGGCACCACTC	314	CTGCTGGCATTCCTCACTTAC	377
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s19	Intron15	0	AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCTTCCTTTCGC	315	ATAGGATGAGGCTCAGCTTGG	378
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s20	Intron21	0	AE100p81p82	XPNPEP2_X21.f1a	GGACTATGGTGACAGCTGGAG	316	CAAGAAGCCCTGTGTTCCTG	379
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s21	Exon21	0	AE100p81p82	XPNPEP2_X21.f1a	GGACTATGGTGACAGCTGGAG	317	CAAGAAGCCCTGTGTTCCTG	380
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	Exon21	0	AE100p85p86	XPNPEP2_X21.f2a	GAGGCTCCAGACTCTCCTGTT	318	TTAGGAATGATGGGTTCACATG	381
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	Exon21	0	AE100p85p86	XPNPEP2_X21.f2a	GAGGCTCCAGACTCTCCTGTT	319	TTAGGAATGATGGGTTCACATG	382
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	Exon21	0	AE100p85p86	XPNPEP2_X21.f2a	GAGGCTCCAGACTCTCCTGTT	320	AAGAAAGCCAAGCTTCTTGGT	383
Bradykinin Receptor B1	BDKRB1	AE103s1	Exon2	0	AE103p13p14	U48231_X2.f3a	CACTTTGCAAGGATTGTGGAG	321	CACCACCAGGAAGATGCTG	384
Bradykinin Receptor B1	BDKRB1	AE103s2	Exon2	0	AE103p5p6	U48231_X2.f1a	TGGCTCTGTGCCAATAAAACT	322	TGGAGGCCAGAAATCCTAAAT	385
Bradykinin Receptor B1	BDKRB1	AE103s3	Exon3	0	AE103p17p18	U48231_X2.f4a	AGGACCAAGGTCTGGGAACT	323	GCTGCCAGGAAGATTAAATGA	386
Bradykinin Receptor B1	BDKRB1	AE103s4	Exon1	0	AE103p1p2	U48231_X1a	ACTTCCCAGACTCAAGGGATC	324	CGTGGTGTGTTCATGCAATT	387
Bradykinin Receptor B1	BDKRB1	AE103s5	Exon3	0	AE103p25p26	U48231_X2.f6a	CGACTAGGTCCTCACCAGACA	325	CTCAGTGTCCAGGGAAATGC	388
Bradykinin Receptor B2	BDKRB2	AE104s1	Intron1	1	AE104p33p34	BDKRB2_X1.f1a	CGACTAGGTCCTCACCAGACA	326	CTCAGTGTCCAGGGAAATGC	389
Bradykinin Receptor B2	BDKRB2	AE104s2	Intron1	1	AE104p33p34	BDKRB2_X1.f1a	GCAGGCAAATACCACTTTCAA	327	CCGAGGTTCTCTGGAGAAAAA	390
Bradykinin Receptor B2	BDKRB2	AE104s3	Intron1	1	AE104p39p40	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	328	CCGAGGTTCTCTGGAGAAAAA	391
Bradykinin Receptor B2	BDKRB2	AE104s4	Intron1	1	AE104p39p40	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	329	CCGAGGTTCTCTGGAGAAAAA	392
Bradykinin Receptor B2	BDKRB2	AE104s5	Intron1	1	AE104p39p40	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	330	CCGAGGTTCTCTGGAGAAAAA	393
Bradykinin Receptor B2	BDKRB2	AE104s6	Intron1	1	AE104p39p40	BDKRB2_X1.f2	GCTCTTTCTGGAAGGTCCACT	331	ATACCAACAGCTTCCCCAGTT	394
Bradykinin Receptor B2	BDKRB2	AE104s7	Intron2	1	AE104p29p30	BDKRB2_X2a	GGTCTCAGCACTGTGATCCTC	332	CAAAGACTCAAGTGGGAACGA	395
Bradykinin Receptor B2	BDKRB2	AE104s8	Exon3	1	AE104p25p26	BDKRB2_X3.f7a	GGTCTCAGCACTGTGATCCTC	333	CAAAGACTCAAGTGGGAACGA	396
Bradykinin Receptor B2	BDKRB2	AE104s9	Exon3	1	AE104p25p26	BDKRB2_X3.f7a	GGTCTCAGCACTGTGATCCTC	334	CAAAGACTCAAGTGGGAACGA	397
Bradykinin Receptor B2	BDKRB2	AE104s10	Exon3	1	AE104p25p26	BDKRB2_X3.f7a	TCTACATGCCAGAAGCCTGTT	335	CCACTCTCCTCTGCCTCAGTA	398
Bradykinin Receptor B2	BDKRB2	AE104s11	Exon3	1	AE104p9p10	BDKRB2_X3.f3a	TCTACATGCCAGAAGCCTGTT	336	CCACTCTCCTCTGCCTCAGTA	399
Bradykinin Receptor B2	BDKRB2	AE104s12	Exon3	1	AE104p9p10	BDKRB2_X3.f3a	TCTACATGCCAGAAGCCTGTT	337	CCACTCTCCTCTGCCTCAGTA	400
Bradykinin Receptor B2	BDKRB2	AE104s13	Exon3	1	AE104p9p10	BDKRB2_X3.f3a	CCTCCAGCTTCTAGCTCAGGT	338	GCAGAATCAGTATTGGGAGCC	401
Bradykinin Receptor B2	BDKRB2	AE104s14	Exon3	1	AE104p21p22	BDKRB2_X3.f6a	GCTTAATGCTTGGGTGATGAA	339	CTAGAATCATAGGCGCAGCAG	402
Bradykinin Receptor B2	BDKRB2	AE104s16	3' Flank	1	AE104p3p4	BDKRB2_X3.f1	GCTTAATGCTTGGGTGATGAA	340	CTAGAATCATAGGCGCAGCAG	403
Bradykinin Receptor B2	BDKRB2	AE104s17	3' Flank	1	AE104p3p4	BDKRB2_X3.f1	CGTGGTCCTCTATGAGCACTT	341	CATCTCCACTAACACCTCGGA	404
Tachykinin Receptor 1	TACR1	AE106s1	Exon1	1	AE106p23p24	TACR1_X1.f1	GGGTATATGTGAGAAATGCTTGC	342	TCATCAGGAATCAAAGGGTTTC	405
Tachykinin Receptor 1	TACR1	AE106s2	Exon2	1	AE106p17p18	TACR1_X2a	CTGGGTTCCAAAGACACTGAA	343	TATGCAGGTGACAAGTCTCCC	406
Tachykinin Receptor 1	TACR1	AE106s3	Intron3	1	AE106p13p14	TACR1_X3a	CTGCAGGAGGCTAATCTGAGA	344	TCCAACTGCTCTTCACGAAGT	407
Tachykinin Receptor 1	TACR1	AE106s4	Exon5	1	AE106p1p2	TACR1_X5.f1a	CTGCAGGAGGCTAATCTGAGA	345	TCCAACTGCTCTTCACGAAGT	408
Tachykinin Receptor 1	TACR1	AE106s5	Exon5	1	AE106p1p2	TACR1_X5.f1a	CTGCAGGAGGCTAATCTGAGA	346	TCCAACTGCTCTTCACGAAGT	409
Tachykinin Receptor 1	TACR1	AE106s6	Exon5	1	AE106p1p2	TACR1_X5.f1a	ACCCATACTGACCCTTTTTGC	347	TAACAAGCTGATGCAGTGGTG	410
Tachykinin Receptor 1	TACR1	AE106s7	Exon5	1	AE106p5p6	TACR1_X5.f2a	AATACCCTCCATTCCAGCCT	348	TGGAGTGACCTAATGCTCCTG	411
C1 Esterase Inhibitor	C1NH	AE105s1	Intron4	0	AE105p17p18	C1NH_X4a	GTCTTCCCATTCTGGGTCCT	349	GGTGGAAATACAGATGGAAGGA	412
C1 Esterase Inhibitor	C1NH	AE105s2	Intron6	0	AE105p25p26	C1NH_X6a	CACTGTTCACCCAGCTGGTAT	350	ACATCTTAGGGATCCCCCTTT	413
C1 Esterase Inhibitor	C1NH	AE105s3	Exon7	0	AE105p29p30	C1NH_X7a	AGATTGCTCATCTGCTGCACT	351	AGTAGTGGGCTGGGTAGGAGA	414
C1 Esterase Inhibitor	C1NH	AE105s4	Exon3	0	AE105p9p10	C1NH_X3.f1a	TTCAGCCACCAAAATAACAGC	352	TGGATTGGTGACTCTTATGGG	415
C1 Esterase Inhibitor	C1NH	AE105s5	Exon3	0	AE105p13p14	C1NH_X3.f2a	GAACCCAGAGAATTCAGGACA	353	GTGGATAGCGGACACCTGAG	416
C1 Esterase Inhibitor	C1NH	AE105s6	Exon8	0	AE105p33p34	C1NH_X8.f1a	GACTACAGCCACGACCTCATG	354	GCTCTCAGAAGCCAGTTCAGA	417
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	Exon4	0	AE107p13p14	KLK1_X4a	GACTACAGCCACGACCTCATG	355	GCTCTCAGAAGCCAGTTCAGA	418
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	Intron4	0	AE107p13p14	KLK1_X4a	GACTACAGCCACGACCTCATG	356	GCTCTCAGAAGCCAGTTCAGA	419
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	Exon3	0	AE107p13p14	KLK1_X4a	GACTACAGCCACGACCTCATG	357	GCTCTCAGAAGCCAGTTCAGA	420
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s4	Intron4	0	AE107p13p14	KLK1_X4a	GCTCCCCAGGCAGAACTT	358	CTGCTGGTGACCTCAGACTTC	421
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s5	3' Flank	0	AE107p17p18	KLK1_X5a	GCTCCCCAGGCAGAACTT	359	CTGCTGGTGACCTCAGACTTC	422
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s6	3' Flank	0	AE107p17p18	KLK1_X5a				

Table VIII(2 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	PCR Amplicon_Name	Target_Name	PCR Left primer	PCR Left primer (SEQ ID NO:)	PCR Right primer	PCR Right primer (SEQ ID NO:)
Bradykinin Receptor B1	BDKRB1	AE103s6	Exon3	0	AE103p9p10	U48231_X2.f2a	GCCTCTGATCTGGTGTTTGTC	707	CTGTGGTCTTGCTATCCTTCG	739
Bradykinin Receptor B1	BDKRB1	AE103s7	Exon3	0	AE103p9p10	U48231_X2.f2a	GCCTCTGATCTGGTGTTTGTC	708	CTGTGGTCTTGCTATCCTTCG	740
Bradykinin Receptor B1	BDKRB1	AE103s8	Exon3	0	AE103p9p10	U48231_X2.f2a	GCCTCTGATCTGGTGTTTGTC	709	CTGTGGTCTTGCTATCCTTCG	741
Bradykinin Receptor B1	BDKRB1	AE103s9	Exon3	0	AE103p13p14	U48231_X2.f3a	CACTTTGCAAGGATTGTGGAG	710	AAGAAAGCCAAGCTTCTTGGT	742
Bradykinin Receptor B2	BDKRB2	AE104s18	Intron1 or Exor	1	AE104p65p66	BDKRB2_X3-5a	GGCAGGGCAGGAATTAGTCT	711	AGATCCAGACAGAGAGGAGGG	743
Bradykinin Receptor B2	BDKRB2	AE104s19	Exon2	1	AE104p65p66	BDKRB2_X3-5a	GGCAGGGCAGGAATTAGTCT	712	AGATCCAGACAGAGAGGAGGG	744
Bradykinin Receptor B2	BDKRB2	AE104s20	5'Flank	1	AE104p89p90	BDKRB2_x1-3a	CTGGGATTTCTTTGTATGCCA	713	AGAGCCTACAGCCAGTTCACA	745
Bradykinin Receptor B2	BDKRB2	AE104s21	5'Flank	1	AE104p89p90	BDKRB2_x1-3a	CTGGGATTTCTTTGTATGCCA	714	AGAGCCTACAGCCAGTTCACA	746
Bradykinin Receptor B2	BDKRB2	AE104s22	5'Flank	1	AE104p87p88	BDKRB2_X1-2	ACCTTCGCTCTCCGCTCT	715	AGAAACCTCCGCCATACATCT	747
Bradykinin Receptor B2	BDKRB2	AE104s23	5'Flank	1	AE104p81p82	BDKRB2_X1-1a	ACGACCACAGGGAAACTTCTC	716	GAGGACGTTTTTGCCGTC	748
Bradykinin Receptor B2	BDKRB2	AE104s24	Exon3	1	AE104p65p66	BDKRB2_X3-5a	GGCAGGGCAGGAATTAGTCT	717	AGATCCAGACAGAGAGGAGGG	749
Bradykinin Receptor B2	BDKRB2	AE104s25	Exon3	1	AE104p65p66	BDKRB2_X3-5a	GGCAGGGCAGGAATTAGTCT	718	AGATCCAGACAGAGAGGAGGG	750
Bradykinin Receptor B2	BDKRB2	AE104s26	Exon3	1	AE104p61p62	BDKRB2_x3-4a	GACCTCCTTGTCCATCAGTGA	719	GGGCTGCTGTGAATTTGTGTA	751
Bradykinin Receptor B2	BDKRB2	AE104s27	Exon3	1	AE104p57p58	BDKRB2_X3-3a	TCCCAGTTACGTCTGCGTAAT	720	GCTGAGTGCACAAGTGAGTTG	752
Bradykinin Receptor B2	BDKRB2	AE104s28	Exon3	1	AE104p53p54	BDKRB2_X3-2a	GCCACCTTCCAATAAACCATT	721	GGGTGATATGGACAGCAGAAG	753
Bradykinin Receptor B2	BDKRB2	AE104s29	Exon3	1	AE104p53p54	BDKRB2_X3-2a	GCCACCTTCCAATAAACCATT	722	GGGTGATATGGACAGCAGAAG	754
Angiotensin Converting Enzyme 2	ACE2	AE109s1	Intron14	1	AE109p25p26	ACE2_x14a	TTAAAAACCCAAAGCCAAAGG	723	TTTCTCGTTTTCCAAAAGCCT	755
Angiotensin Converting Enzyme 2	ACE2	AE109s2	Intron12	1	AE109p29p30	ACE2_x13a	CACCATAGCAGAGAAAGAAGCA	724	GCCAAGTCAAAGAGAAGAAACC	756
Angiotensin Converting Enzyme 2	ACE2	AE109s3	Intron13	1	AE109p29p30	ACE2_x13a	CACCATAGCAGAGAAAGAAGCA	725	GCCAAGTCAAAGAGAAGAAACC	757
Angiotensin Converting Enzyme 2	ACE2	AE109s4	Intron3	1	AE109p69p70	ACE2_x3a	GTAAGGTTGGCAGACATCAGG	726	AAAAATCATGTGGTCAAAAGGA	758
Angiotensin Converting Enzyme 2	ACE2	AE109s5	Intron2	1	AE109p69p70	ACE2_x3a	GTAAGGTTGGCAGACATCAGG	727	AAAAATCATGTGGTCAAAAGGA	759
Angiotensin Converting Enzyme 2	ACE2	AE109s6	Intron16	1	AE109p17p18	ACE2_x16a	CTGTGGGATCCTTCTGGAATT	728	CAATTACATCCTCTCATTGTTTGC	760
Angiotensin Converting Enzyme 2	ACE2	AE109s7	Exon16	1	AE109p17p18	ACE2_x16a	CTGTGGGATCCTTCTGGAATT	729	CAATTACATCCTCTCATTGTTTGC	761
Protease Inhibitor 4	PI4	AE110s1	Intron1	0	AE110p21p22	PI4_X2a	GGACATCTTGATGGGCTCATA	730	TGGGGCACTGTCTTTCATTAG	762
Protease Inhibitor 4	PI4	AE110s2	Exon2	0	AE110p21p22	PI4_X2a	GGACATCTTGATGGGCTCATA	731	TGGGGCACTGTCTTTCATTAG	763
Protease Inhibitor 4	PI4	AE110s3	Intron2	0	AE110p25p26	PI4_X3a	GCCTGGGTACAAAGGAACCT	732	CCGAGTTCTCTAGGGATTGCT	764
Protease Inhibitor 4	PI4	AE110s4	Intron2	0	AE110p25p26	PI4_X3a	GCCTGGGTACAAAGGAACCT	733	CCGAGTTCTCTAGGGATTGCT	765
Protease Inhibitor 4	PI4	AE110s5	Exon1	0	AE110p17p18	PI4_X1.f5a	AAGAACATCTTTTTCTCCCCG	734	CAACAAATTAGTGGGTTGGAGG	766
Protease Inhibitor 4	PI4	AE110s6	5'Flank	0	AE110p5p6	PI4_X1.f2a	TAGAAGCTTTTTGGCCTGACA	735	TGAGCTCTGCACAGCACTAGA	767
Protease Inhibitor 4	PI4	AE110s7	5'Flank	0	AE110p5p6	PI4_X1.f2a	TAGAAGCTTTTTGGCCTGACA	736	TGAGCTCTGCACAGCACTAGA	768
Protease Inhibitor 4	PI4	AE110s8	5'Flank	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	737	TGTTACCCCGTACAGACAAGG	769
Protease Inhibitor 4	PI4	AE110s9	5'Flank	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	738	TGTTACCCCGTACAGACAAGG	770
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	Intron11	0	AE100p45p46	XPNPEP2_X12a	TTTTCAAAGCTCCACATCCTG	962	TCGAGTTGTCCTGCTTTCAG	988
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s25	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	963	CAGCTCTCAGGCCTTTTCATT	989
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s26	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	964	CAGCTCTCAGGCCTTTTCATT	990
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s27	Intron7	0	AE100p29p30	XPNPEP2_X8a	GGCCCATGTCATTAATGAGTAC	965	TCAGGGCTACCTTTTGTCCTT	991
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s28	Exon21	0	AE100p93p94	XPNPEP2_X21.f4a	GAACTTTCCAAAGTGCAGCC	966	ACACATACTCTCAAGCCCACG	992
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s29	Exon21	0	AE100p93p94	XPNPEP2_X21.f4a	GAACTTTCCAAAGTGCAGCC	967	ACACATACTCTCAAGCCCACG	993
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s30	Exon6	0	AE100p17p18	XPNPEP2_X5a	GAGAATCTCTTTCCAGAGGCC	968	TGCACGCTCTCACCTATACCT	994
Bradykinin Receptor B1	BDKRB1	AE103s10	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	969	CGTGGTGTGTTCATGCAATT	995
Bradykinin Receptor B1	BDKRB1	AE103s11	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	970	CGTGGTGTGTTCATGCAATT	996
Bradykinin Receptor B1	BDKRB1	AE103s12	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	971	CGTGGTGTGTTCATGCAATT	997
Bradykinin Receptor B1	BDKRB1	AE103s13	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	972	CGTGGTGTGTTCATGCAATT	998
Bradykinin Receptor B1	BDKRB1	AE103s14	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	973	CGTGGTGTGTTCATGCAATT	999
Bradykinin Receptor B2	BDKRB2	AE104s30	Exon3	1	AE104p53p54	BDKRB2_X3.f2a	GCCACCTTCCAATAAACCATT	974	GGGTGATATGGACAGCAGAAG	1000
Bradykinin Receptor B2	BDKRB2	AE104s31	Exon3	1	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	975	GAGGACGTTTTTGCCGTC	1001
Bradykinin Receptor B2	BDKRB2	AE104s32	Intron1	1	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	976	GAGGACGTTTTTGCCGTC	1002
Bradykinin Receptor B2	BDKRB2	AE104s33	Intron1	1	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	977	GAGGACGTTTTTGCCGTC	1003
Bradykinin Receptor B2	BDKRB2	AE104s34	Exon3	1	AE104p73p74	BDKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	978	TTTTTGTCCTTCCCTTGTGAC	1004
Bradykinin Receptor B2	BDKRB2	AE104s35	Exon3	1	AE104p73p74	BDKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	979	TTTTTGTCCTTCCCTTGTGAC	1005
Bradykinin Receptor B2	BDKRB2	AE104s36	Exon3	1	AE104p73p74	BDKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	980	TTTTTGTCCTTCCCTTGTGAC	1006
Protease Inhibitor 4	PI4	AE110s10	Exon4	0	AE110p29p30	PI4_X4a	ATTTCTGGCTCTCGCAGTCTT	981	CCTTTCCAGAGGCAGAAACTT	1007
Protease Inhibitor 4	PI4	AE110s11	Exon1	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	982	TGTTACCCCGTACAGACAAGG	1008
Protease Inhibitor 4	PI4	AE110s12	5' Flank	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	983	TGTTACCCCGTACAGACAAGG	1009
Tachykinin Receptor 1	TACR1	AE106s8	Intron4	1	AE106p9p10	TACR1_X4a	AAGTTAGCTGCAGTCCCCACT	984	GCTTCATCCCATACTGTGCA	1010
Tachykinin Receptor 1	TACR1	AE106s9	Intron3	1	AE106p13p14	TACR1_X3a	CTGGGTTCCAAAGACACTGAA	985	TATGCAGGTGACAAGTCTCCC	1011
Angiotensin Converting Enzyme 2	ACE2	AE109s8	Intron13	1	AE109p29p30	ACE2_X13a	CACCATAGCAGAGAAAGAAGCA	986	GCCAAGTCAAAGAGAAGAAACC	1012
Angiotensin Converting Enzyme 2	ACE2	AE109s9	Intron6	1	AE109p57p58	ACE2_X6a	CAAAATGCGATTTCTACAATGTT	987	TGGAATGGAAATTAGAATTGGTT	1013

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GENE_DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	Target_Name	Forward sequencing primer	forward seq name	Forward sequencing primer (SEQ ID NO:)	Reverse sequencing primer	reverse seq name	Reverse sequencing primer (SEQ ID NO:)
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	Exon20	0	XPNPEP2_X20a	AGTTCCTCCTCCTCCCTCACT	AE100p79	423	AGGCTGGTCTGACTGGAAAGT	AE100p80	486
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	Intron3	0	XPNPEP2_X3a	CAGTAACATCAGTTGCCACCC	AE100p11	424	TCCTGTTTGTGGTCTCTGACC	AE100p12	487
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s3	Intron15	0	XPNPEP2_X15a	CACTTGTGGAAAGCACACAGA	AE100p59	425	TGTCAGTGGCCTGAAATATCC	AE100p60	488
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s4	Intron15	0	XPNPEP2_X15a	CACTTGTGGAAAGCACACAGA	AE100p59	426	TGTCAGTGGCCTGAAATATCC	AE100p60	489
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s5	Intron1	0	XPNPEP2_X1a	CCTCTGTCTCTGAGATCTTTGGA	AE100p3	427	AGAGGTCAGAGCTGCCTTCC	AE100p4	490
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s6	Intron7	0	XPNPEP2_X7a	GCAAAGGGAACCAGGACTAAC	AE100p27	428	TAAACAAGCATCCCAGGTGAC	AE100p28	491
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	Intron7	0	XPNPEP2_X7a	GCAAAGGGAACCAGGACTAAC	AE100p27	429	TAAACAAGCATCCCAGGTGAC	AE100p28	492
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	Intron10	0	XPNPEP2_X10a	CTTTGCATCCTTAGCAGATGC	AE100p39	430	AAGAAGGGAACTCACTGCACA	AE100p40	493
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	Intron10	0	XPNPEP2_X10a	CTTTGCATCCTTAGCAGATGC	AE100p39	431	AAGAAGGGAACTCACTGCACA	AE100p40	494
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	Intron7	0	XPNPEP2_X7a	GCAAAGGGAACCAGGACTAAC	AE100p27	432	TAAACAAGCATCCCAGGTGAC	AE100p28	495
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	433	GCAACTCCCTACTCCACACTG	AE100p52	496
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	434	GCAACTCCCTACTCCACACTG	AE100p52	497
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	435	GCAACTCCCTACTCCACACTG	AE100p52	498
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	Exon1	0	XPNPEP2_X1a	CCTCTGTCTCTGAGATCTTTGGA	AE100p3	436	AGAGGTCAGAGCTGCCTTCC	AE100p4	499
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	Exon1	0	XPNPEP2_X1a	CCTCTGTCTCTGAGATCTTTGGA	AE100p3	437	AGAGGTCAGAGCTGCCTTCC	AE100p4	500
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s16	Intron8	0	XPNPEP2_X8a	AGGGTTTCGCTGCTTTTTAAG	AE100p31	438	CTTACCCTTCTTGGTTCCCAC	AE100p32	501
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s17	Intron17	0	XPNPEP2_X17a	CAAGGTGGACAGTCTTCGGTA	AE100p67	439	AGCTGGGTAACCTTGGGTAGA	AE100p68	502
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s18	Intron17	0	XPNPEP2_X17a	CAAGGTGGACAGTCTTCGGTA	AE100p67	440	AGCTGGGTAACCTTGGGTAGA	AE100p68	503
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s19	Intron15	0	XPNPEP2_X15a	CACTTGTGGAAAGCACACAGA	AE100p59	441	TGTCAGTGGCCTGAAATATCC	AE100p60	504
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s20	Intron21	0	XPNPEP2_X21.f1a	CAAGACTTCACCTCTTGGCAG	AE100p83	442	TGGGACCTTCTCCATAGGTCT	AE100p84	505
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s21	Exon21	0	XPNPEP2_X21.f1a	CAAGACTTCACCTCTTGGCAG	AE100p83	443	TGGGACCTTCTCCATAGGTCT	AE100p84	506
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	Exon21	0	XPNPEP2_X21.f2a	ACTGAACATACCCCAAGAGCC	AE100p87	444	GGTTGATGTTTCATGCCCTG	AE100p88	507
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	Exon21	0	XPNPEP2_X21.f2a	ACTGAACATACCCCAAGAGCC	AE100p87	445	GGTTGATGTTTCATGCCCTG	AE100p88	508
Bradykinin Receptor B1	BDKRB1	AE103s1	Exon2	0	U48231_X2.f3a	TCTGGGTTTCCTCCTACCACT	AE103p15	446	TCAATGCTGTTTTAATTCCGC	AE103p16	509
Bradykinin Receptor B1	BDKRB1	AE103s2	Exon2	0	U48231_X2.f1a	GACAGGTTGGTTTGGCTCATA	AE103p7	447	ATGAACAAATTGGCCTTGATG	AE103p8	510
Bradykinin Receptor B1	BDKRB1	AE103s3	Exon3	0	U48231_X2.f4a	CACCCCTAAAAGTCTTGCTCC	AE103p19	448	AGGACCCATTCCTTCTGGAG	AE103p20	511
Bradykinin Receptor B1	BDKRB1	AE103s4	Exon1	0	U48231_X1a	GCCTGGAACACAGACCATTAA	AE103p3	449	GGATCAGATGAACCCAGGAGT	AE103p4	512
Bradykinin Receptor B1	BDKRB1	AE103s5	Exon3	0	U48231_X2.f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	450	TGGTGTGTTCATGCAATTTCT	AE103p28	513
Bradykinin Receptor B2	BDKRB2	AE104s1	Intron1	1	BDKRB2_X1.f1a	GCACCGAGAGCAATAAATGTC	AE104p35	451	CTTTGGGATTCCCTCCCTT	AE104p36	514
Bradykinin Receptor B2	BDKRB2	AE104s2	Intron1	1	BDKRB2_X1.f1a	GCACCGAGAGCAATAAATGTC	AE104p35	452	CTTTGGGATTCCCTCCCTT	AE104p36	515
Bradykinin Receptor B2	BDKRB2	AE104s3	Intron1	1	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	AE104p39	453	CCGAGGTTCTCTGGAGAAAAA	AE104p40	516
Bradykinin Receptor B2	BDKRB2	AE104s4	Intron1	1	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	AE104p39	454	CCGAGGTTCTCTGGAGAAAAA	AE104p40	517
Bradykinin Receptor B2	BDKRB2	AE104s5	Intron1	1	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	AE104p39	455	CCGAGGTTCTCTGGAGAAAAA	AE104p40	518
Bradykinin Receptor B2	BDKRB2	AE104s6	Intron1	1	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	AE104p39	456	CCGAGGTTCTCTGGAGAAAAA	AE104p40	519
Bradykinin Receptor B2	BDKRB2	AE104s7	Intron2	1	BDKRB2_X2a	GAGCTGAACTACGAGTCACGG	AE104p31	457	GGTCCACTTGTCCTCCTTCTT	AE104p32	520
Bradykinin Receptor B2	BDKRB2	AE104s8	Exon3	1	BDKRB2_X3.f7a	ATCTTCCTCTGCCTCATCACA	AE104p27	458	CAGAAAGCTGTTCGACGAGAC	AE104p28	521
Bradykinin Receptor B2	BDKRB2	AE104s9	Exon3	1	BDKRB2_X3.f7a	ATCTTCCTCTGCCTCATCACA	AE104p27	459	CAGAAAGCTGTTCGACGAGAC	AE104p28	522
Bradykinin Receptor B2	BDKRB2	AE104s10	Exon3	1	BDKRB2_X3.f7a	ATCTTCCTCTGCCTCATCACA	AE104p27	460	CAGAAAGCTGTTCGACGAGAC	AE104p28	523
Bradykinin Receptor B2	BDKRB2	AE104s11	Exon3	1	BDKRB2_X3.f3a	AAAGGCTTCTGAGTGTGCAAG	AE104p11	461	TGGAGGAAGAAAACAGGTGAA	AE104p12	524
Bradykinin Receptor B2	BDKRB2	AE104s12	Exon3	1	BDKRB2_X3.f3a	AAAGGCTTCTGAGTGTGCAAG	AE104p11	462	TGGAGGAAGAAAACAGGTGAA	AE104p12	525
Bradykinin Receptor B2	BDKRB2	AE104s13	Exon3	1	BDKRB2_X3.f3a	AAAGGCTTCTGAGTGTGCAAG	AE104p11	463	TGGAGGAAGAAAACAGGTGAA	AE104p12	526
Bradykinin Receptor B2	BDKRB2	AE104s14	Exon3	1	BDKRB2_X3.f6a	CAGGTTCTAGCCCTTCTTGGT	AE104p23	464	ACACAGTAGGTGCTCATTGGC	AE104p24	527
Bradykinin Receptor B2	BDKRB2	AE104s16	3' Flank	1	BDKRB2_X3.f1	TGGGAGTATGAAACAAGTGGC	AE104p5	465	TGGATGAGGTTTTTGCATAGC	AE104p6	528
Bradykinin Receptor B2	BDKRB2	AE104s17	3' Flank	1	BDKRB2_X3.f1	TGGGAGTATGAAACAAGTGGC	AE104p5	466	TGGATGAGGTTTTTGCATAGC	AE104p6	529
Tachykinin Receptor 1	TACR1	AE106s1	Exon1	1	TACR1_X1.f1	TTGTGGGCTAAGATGATCCAC	AE106p25	467	TTACCGCAAGAGAGATGCTGT	AE106p26	530
Tachykinin Receptor 1	TACR1	AE106s2	Exon2	1	TACR1_X2a	GAAAGAAAGAGCAAGAAGGGG	AE106p19	468	TGGCAGGAAAAATATGGAATC	AE106p20	531
Tachykinin Receptor 1	TACR1	AE106s3	Intron3	1	TACR1_X3a	CCTCTCCTCCTCTCTGTTGCT	AE106p15	469	GTAGCTGCCAAACCTTGACTG	AE106p16	532
Tachykinin Receptor 1	TACR1	AE106s4	Exon5	1	TACR1_X5.f1a	GGCTCCAGGAAAATGAGTCTT	AE106p3	470	GAGAGCTTCAGCTTCTCCTCC	AE106p4	533
Tachykinin Receptor 1	TACR1	AE106s5	Exon5	1	TACR1_X5.f1a	GGCTCCAGGAAAATGAGTCTT	AE106p3	471	GAGAGCTTCAGCTTCTCCTCC	AE106p4	534
Tachykinin Receptor 1	TACR1	AE106s6	Exon5	1	TACR1_X5.f1a	GGCTCCAGGAAAATGAGTCTT	AE106p3	472	GAGAGCTTCAGCTTCTCCTCC	AE106p4	535
Tachykinin Receptor 1	TACR1	AE106s7	Exon5	1	TACR1_X5.f2a	ATGGTTCCAGATGAAGGGAAT	AE106p7	473	AGGGTCACCTCTTCATCTGCT	AE106p8	536
C1 Esterase Inhibitor	C1NH	AE105s1	Intron4	0	C1NH_X4a	CCGACTCATCCTGCAAGTATC	AE105p19	474	TCTGCAGTCCATCCCTGATAC	AE105p20	537
C1 Esterase Inhibitor	C1NH	AE105s2	Intron6	0	C1NH_X6a	CCCCAAGTTCTACAATCGGAT	AE105p27	475	ACCCCAAAATGATGGGACTAC	AE105p28	538
C1 Esterase Inhibitor	C1NH	AE105s3	Exon7	0	C1NH_X7a	AAGCCTGGAAGCTTAGGTCTG	AE105p31	476	CCTGGGAGTAACCCTAAGCTG	AE105p32	539
C1 Esterase Inhibitor	C1NH	AE105s4	Exon3	0	C1NH_X3.f1a	TTTCCACATCCACACCTTCTC	AE105p11	477	ATCTGTTGGGAGCTGGGTAGT	AE105p12	540
C1 Esterase Inhibitor	C1NH	AE105s5	Exon3	0	C1NH_X3.f2a	ATACCACTGATGAACCCACCA	AE105p15	478	GTCCAACAAATGACCTGGAGA	AE105p16	541
C1 Esterase Inhibitor	C1NH	AE105s6	Exon8	0	C1NH_X8.f1a	CTCCATCAGCTGAGGGTATCA	AE105p35	479	GAGCTGAGGCTGGAGAGGTAG	AE105p36	542
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	Exon4	0	KLK1_X4a	CCTGACAGAGCCTGCTGATAC	AE107p15	480	CCTCACCACACAGGTGTCTTT	AE107p16	543
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	Intron4	0	KLK1_X4a	CCTGACAGAGCCTGCTGATAC	AE107p15	481	CCTCACCACACAGGTGTCTTT	AE107p16	544
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	Exon3	0	KLK1_X4a	CCTGACAGAGCCTGCTGATAC	AE107p15	482	CCTCACCACACAGGTGTCTTT	AE107p16	545
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s4	Intron4	0	KLK1_X4a	CCTGACAGAGCCTGCTGATAC	AE107p15	483	CCTCACCACACAGGTGTCTTT	AE107p16	546
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s5	3' Flank	0	KLK1_X5a	CCCCGTAGACCTTTCTCACTC	AE107p19	484	GTGCACCACATCTGGAAAGAT	AE107p20	547
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s6	3' Flank	0	KLK1_X5a	CCCCGTAGACCTTTCTCACTC	AE107p19	485	GTGCACCACATCTGGAAAGAT	AE107p20	548
Bradykinin Receptor B1	BDKRB1	AE103s6	Exon3	0	U48231_X2.f2a	CCCTTCTGGGCAGAGAATATC	AE103p11	771	CACTCTTGTCCTGCTGACCTC	AE103p12	803
Bradykinin Receptor B1	BDKRB1	AE103s7	Exon3	0	U48231_X2.f2a	CCCTTCTGGGCAGAGAATATC	AE103p11	772	CACTCTTGTCCTGCTGACCTC	AE103p12	804
Bradykinin Receptor B1	BDKRB1	AE103s8	Exon3	0	U48231_X2.f2a	CCCTTCTGGGCAGAGAATATC	AE103p11	773	CACTCTTGTCCTGCTGACCTC	AE103p12	805
Bradykinin Receptor B1	BDKRB1	AE103s9	Exon3	0	U48231_X2.f3a	TCTGGGTTTCCTCCTACCACT	AE103p15	774	TCAATGCTGTTTTAATTCCGC	AE103p16	806
Bradykinin Receptor B2	BDKRB2	AE104s18	tron1 or Exo	1	BDKRB2_X3-5a	GGTGTTTTACCGGAGACATCA	AE104p67	775	GGTTGTGCTGCTGCTATTCAT	AE104p68	807
Bradykinin Receptor B2	BDKRB2	AE104s19	Exon2	1	BDKRB2_X3-5a	GGTGTTTTACCGGAGACATCA	AE104p67	776	GGTTGTGCTGCTGCTATTCAT	AE104p68	808
Bradykinin Receptor B2	BDKRB2	AE104s20	5'Flank	1	BDKRB2_x1-3a	CAGAAGCTGTCCTGTTTCCTG	AE104p91	777	GCCACCCATAAACTGATCTGA	AE104p92	809
Bradykinin Receptor B2	BDKRB2	AE104s21	5'Flank	1	BDKRB2_x1-3a	CAGAAGCTGTCCTGTTTCCTG	AE104p91	778	GCCACCCATAAACTGATCTGA	AE104p92	810
Bradykinin Receptor B2	BDKRB2	AE104s22	5'Flank	1	BDKRB2_X1-2	ACCTTCGCTCTCCGCTCT	AE104p87	779	AGAAACCTCCGCCATACATCT	AE104p88	811
Bradykinin Receptor B2	BDKRB2	AE104s23	5'Flank	1	BDKRB2_X1-1a	CTCTGTGCTGGGACAGTTTGT	AE104p83	780	GAGCTACGCAAACATGGAAAT	AE104p84	812
Bradykinin Receptor B2	BDKRB2	AE104s24	Exon3	1	BDKRB2_X3-5a	GGTGTTTTACCGGAGACATCA	AE104p67	781	GGTTGTGCTGCTGCTATTCAT	AE104p68	813
Bradykinin Receptor B2	BDKRB2	AE104s25	Exon3	1	BDKRB2_X3-5a	GGTGTTTTACCGGAGACATCA	AE104p67	782	GGTTGTGCTGCTGCTATTCAT	AE104p68	814
Bradykinin Receptor B2	BDKRB2	AE104s26	Exon3	1	BDKRB2_x3-4a	AATCCTGGTCTCCAGGTTGTT	AE104p63	783	TGAGGGACAGTTGCTTTTCAG	AE104p64	815
Bradykinin Receptor B2	BDKRB2	AE104s27	Exon3	1	BDKRB2_X3-3a	ACGTAGCACCCTTTGCTTTTC	AE104p59	784	TGCCCTGGGTTTCTTTAATCT	AE104p60	816

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Bradykinin Receptor B2	BDKRB2	AE104s28	Exon3	1	BDKRB2_ X3-2a	TTGCTGAGACAGGAACAGTCC	AE104p55	785	TATTGCACAACCATCTGTCCC	AE104p56	817
Bradykinin Receptor B2	BDKRB2	AE104s29	Exon3	1	BDKRB2_ X3-2a	TTGCTGAGACAGGAACAGTCC	AE104p55	786	TATTGCACAACCATCTGTCCC	AE104p56	818
Angiotensin Converting Enzyme 2	ACE2	AE109s1	Intron14	1	ACE2_x14a	TTTTGAAAAGAACCACATGGC	AE109p27	787	AGTGGGATCTTTGGAGGAAAA	AE109p28	819
Angiotensin Converting Enzyme 2	ACE2	AE109s2	Intron12	1	ACE2_x13a	CAGCTGTGTCACAAGTCCTCA	AE109p31	788	ACATCTGGAACCCCTCAAAAG	AE109p32	820
Angiotensin Converting Enzyme 2	ACE2	AE109s3	Intron13	1	ACE2_x13a	CAGCTGTGTCACAAGTCCTCA	AE109p31	789	ACATCTGGAACCCCTCAAAAG	AE109p32	821
Angiotensin Converting Enzyme 2	ACE2	AE109s4	Intron3	1	ACE2_x3a	TCATTCATGTCCTTGCCCTTA	AE109p71	790	TCTTCAGCAAAATTTCCATTGTT	AE109p72	822
Angiotensin Converting Enzyme 2	ACE2	AE109s5	Intron2	1	ACE2_x3a	TCATTCATGTCCTTGCCCTTA	AE109p71	791	TCTTCAGCAAAATTTCCATTGTT	AE109p72	823
Angiotensin Converting Enzyme 2	ACE2	AE109s6	Intron16	1	ACE2_x16a	GCACACAGGAAGAACACACAA	AE109p19	792	CCTCCCCCATGTCTCTCTATC	AE109p20	824
Angiotensin Converting Enzyme 2	ACE2	AE109s7	Exon16	1	ACE2_x16a	GCACACAGGAAGAACACACAA	AE109p19	793	CCTCCCCCATGTCTCTCTATC	AE109p20	825
Protease Inhibitor 4	PI4	AE110s1	Intron1	0	PI4_X2a	GATCTGGAGCGACTGTTTCTG	AE110p23	794	CACACTGATTACCTCTTCCGC	AE110p24	826
Protease Inhibitor 4	PI4	AE110s2	Exon2	0	PI4_X2a	GATCTGGAGCGACTGTTTCTG	AE110p23	795	CACACTGATTACCTCTTCCGC	AE110p24	827
Protease Inhibitor 4	PI4	AE110s3	Intron2	0	PI4_X3a	CTTTCAACATCCATTTGTGGG	AE110p27	796	ACTTTGGATGCCTCCAGTTTT	AE110p28	828
Protease Inhibitor 4	PI4	AE110s4	Intron2	0	PI4_X3a	CTTTCAACATCCATTTGTGGG	AE110p27	797	ACTTTGGATGCCTCCAGTTTT	AE110p28	829
Protease Inhibitor 4	PI4	AE110s5	Exon1	0	PI4_X1.f5a	CTACGCCATGCTTTCCCTG	AE110p19	798	CGGTGGTGTGGATTTAGCATA	AE110p20	830
Protease Inhibitor 4	PI4	AE110s6	5'Flank	0	PI4_X1.f2a	TTGGGGGAGAAACTGGAGTAT	AE110p7	799	CCAACAGAGCAGGAAATGAAG	AE110p8	831
Protease Inhibitor 4	PI4	AE110s7	5'Flank	0	PI4_X1.f2a	TTGGGGGAGAAACTGGAGTAT	AE110p7	800	CCAACAGAGCAGGAAATGAAG	AE110p8	832
Protease Inhibitor 4	PI4	AE110s8	5'Flank	0	PI4_X1.f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	801	TAAGTGACCTGCCCAAAGTTG	AE110p4	833
Protease Inhibitor 4	PI4	AE110s9	5'Flank	0	PI4_X1.f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	802	TAAGTGACCTGCCCAAAGTTG	AE110p4	834
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	Intron11	0	XPNPEP2_X12a	ATCTCCATCATCTTGGAGCCT	AE100p47	1014	ACCCAAGAACCTGTCACTCCT	AE100p48	1040
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s25	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	1015	GCAACTCCCTACTCCACACTG	AE100p52	1041
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s26	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	1016	GCAACTCCCTACTCCACACTG	AE100p52	1042
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s27	Intron7	0	XPNPEP2_X8a	AGGGTTTCGCTGCTTTTTAAG	AE100p31	1017	CTTACCCTTCTTGGTTCCCAC	AE100p32	1043
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s28	Exon21	0	XPNPEP2_X21.f4a	CAATGCTGTTAAATCCTCCCA	AE100p95	1018	CTCACCCTCTCTTCTTCCTCC	AE100p96	1044
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s29	Exon21	0	XPNPEP2_X21.f4a	CAATGCTGTTAAATCCTCCCA	AE100p95	1019	CTCACCCTCTCTTCTTCCTCC	AE100p96	1045
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s30	Exon6	0	XPNPEP2_X5a	ACATCCATCAGCTAATGCCAC	AE100p19	1020	GAACCTAGTCCAGGTCCCAAG	AE100p20	1046
Bradykinin Receptor B1	BDKRB1	AE103s10	Exon3	0	U48231_X2.f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1021	TGGTGTGTTCATGCAATTTCT	AE103p28	1047
Bradykinin Receptor B1	BDKRB1	AE103s11	Exon3	0	U48231_X2.f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1022	TGGTGTGTTCATGCAATTTCT	AE103p28	1048
Bradykinin Receptor B1	BDKRB1	AE103s12	Exon3	0	U48231_X2.f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1023	TGGTGTGTTCATGCAATTTCT	AE103p28	1049
Bradykinin Receptor B1	BDKRB1	AE103s13	Exon3	0	U48231_X2.f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1024	TGGTGTGTTCATGCAATTTCT	AE103p28	1050
Bradykinin Receptor B1	BDKRB1	AE103s14	Exon3	0	U48231_X2.f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1025	TGGTGTGTTCATGCAATTTCT	AE103p28	1051
Bradykinin Receptor B2	BDKRB2	AE104s30	Exon3	1	BDKRB2_X3.f2a	TTGCTGAGACAGGAACAGTCC	AE104p55	1026	TATTGCACAACCATCTGTCCC	AE104p56	1052
Bradykinin Receptor B2	BDKRB2	AE104s31	Exon3	1	BDKRB2_X1.f1a	CTCTGTGCTGGGACAGTTTGT	AE104p83	1027	GAGCTACGCAAACATGGAAAT	AE104p84	1053
Bradykinin Receptor B2	BDKRB2	AE104s32	Intron1	1	BDKRB2_X1.f1a	CTCTGTGCTGGGACAGTTTGT	AE104p83	1028	GAGCTACGCAAACATGGAAAT	AE104p84	1054
Bradykinin Receptor B2	BDKRB2	AE104s33	Intron1	1	BDKRB2_X1.f1a	CTCTGTGCTGGGACAGTTTGT	AE104p83	1029	GAGCTACGCAAACATGGAAAT	AE104p84	1055
Bradykinin Receptor B2	BDKRB2	AE104s34	Exon3	1	BDKRB2_X3.f7a	CCCAGATCACCAAGCTGTAGA	AE104p75	1030	CTTTTCCACTTTCTTTCAGCG	AE104p76	1056
Bradykinin Receptor B2	BDKRB2	AE104s35	Exon3	1	BDKRB2_X3.f7a	CCCAGATCACCAAGCTGTAGA	AE104p75	1031	CTTTTCCACTTTCTTTCAGCG	AE104p76	1057
Bradykinin Receptor B2	BDKRB2	AE104s36	Exon3	1	BDKRB2_X3.f7a	CCCAGATCACCAAGCTGTAGA	AE104p75	1032	CTTTTCCACTTTCTTTCAGCG	AE104p76	1058
Protease Inhibitor 4	PI4	AE110s10	Exon4	0	PI4_X4a	TCTCTTGCTGGCTTGGAGATA	AE110p31	1033	CAGGGTGTGGAATGTCCAG	AE110p32	1059
Protease Inhibitor 4	PI4	AE110s11	Exon1	0	PI4_X1.f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	1034	TAAGTGACCTGCCCAAAGTTG	AE110p4	1060
Protease Inhibitor 4	PI4	AE110s12	5' Flank	0	PI4_X1.f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	1035	TAAGTGACCTGCCCAAAGTTG	AE110p4	1061
Tachykinin Receptor 1	TACR1	AE106s8	Intron4	1	TACR1_X4a	TGTCCCTCTTGTCTCACAGCT	AE106p11	1036	CTCACCTGTCTCACCCTCTTG	AE106p12	1062
Tachykinin Receptor 1	TACR1	AE106s9	Intron3	1	TACR1_X3a	CCTCTCCTCCTCTCTGTTGCT	AE106p15	1037	GTAGCTGCCAAACCTTGACTG	AE106p16	1063
Angiotensin Converting Enzyme 2	ACE2	AE109s8	Intron13	1	ACE2_X13a	CAGCTGTGTCACAAGTCCTCA	AE109p31	1038	ACATCTGGAACCCCTCAAAAG	AE109p32	1064
Angiotensin Converting Enzyme 2	ACE2	AE109s9	Intron6	1	ACE2_X6a	TAAGGCTCACTCAAAAAGGCA	AE109p59	1039	TCTTCCTGGGCTTTTCAGATT	AE109p60	1065

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPIT	ORCHID_SNPIT (SEQ ID NO:)
AE100s1	TATCATTTGTGCCCTATGACCG	1066	CAGGGTCAGGGAGAAGGC	1154	CCTCATCGATGTCNGCCTGCTGTCTCC	1242
AE100s10	AAACTTCATCATCAGAGGTACCAAAG	1067	GAGGACATTTTGATTCAGACTCCTC	1155	GTGGTTTGCAAACCTTAGCATGCAC	1243
AE100s11	ATAGAATGACTTCCTCCAGAGGGA	1068	CAGCCTAACCCTGYACTGGG	1156	TGGAAGCCCAGNCCCCAGAGGT	1244
AE100s12	TCCAGAGGGACTGGCCTG	1069	GAAGGGCAGCCTAACCCTG	1157	AGCCCAGGCCCCAGAGGTYCTCCCA	1245
AE100s13	ATAGAATGACTTCCTCCAGAGGGA	1070	GCTGAGAAGGGGAGAGAATGTT	1158	AATGTTGAGAANGNCAGCCTAACCCTG	1246
AE100s14	N/A	N/A	N/A	N/A	N/A	N/A
AE100s15	ACCCTCTGTCTGCTCGAG	1071	GATGGAGGGACAAGGGAG	1159	CCCGGSCTCTTCCTTCANGCNTTTCCT	1247
AE100s16	AAAGAAGGAAGGAAGGAAAGGAA	1072	GTGTAGGAATAGAAGAAGGGGTTATAGG	1160	AGAAAAGCTTGNCTCAGGCAGATCAGC	1248
AE100s17	N/A	N/A	N/A	N/A	N/A	N/A
AE100s18	AACACAGCAAGACCCCTCTCA	1073	GATCCCAGAGCATCTCTATGAGC	1161	TACCTAAATAAATAATAAAAGCCAG	1249
AE100s19	N/A	N/A	N/A	N/A	N/A	N/A
AE100s2	ATAGAATTTGCAGGGCAGGG	1074	GTATCTTTTGCAGTTCAACTCCCC	1162	GCAACAAGTCTCCTTTNCAGAACAGTC	1250
AE100s20	TACCACAACAGGGGACTGG	1075	GATTCAGGTACTGGAGCTGCG	1163	AGACTTCACCTCTTGGCANCTTGGCTT	1251
AE100s21	N/A	N/A	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A	N/A	N/A
AE100s23	TTTGCCTAAGGACACACAAATTT	1076	GAGGTGGGCTCAGGGACT	1164	CTGCATGTTGCTGAAGGGTGAAAGA	1252
AE100s24	CGCTATCTGATCTCCATCATCT	1077	CCGCACCTGGAGTTGGGG	1165	TTNGAGCCTGTGGCTNCAACCAGACCT	1253
AE100s25	N/A	N/A	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A	N/A	N/A
AE100s27	ACAAGTAAGAGTTTGTTTGAGGAAAGG	1078	GAGCCCCAAAAAAGTGTAAGTGA	1166	TTACCCTANGGCTGACCTNCCAGGAAC	1254
AE100s28	N/A	N/A	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A	N/A	N/A
AE100s3	N/A	N/A	N/A	N/A	N/A	N/A
AE100s30	TATCTTTCTTTCAGTTGGCACCA	1079	CAATGGACAAGAGGAAGGGG	1167	TCACCTGGCTCCTCACCGAGATTCC	1255
AE100s4	TCCCTGCTGCTTCCCCGG	1080	AATATTTGTGCACTGATTTACCAGAATAG	1168	TATTTCAGNCCACTGACANGGCCTCAG	1256
AE100s5	N/A	N/A	N/A	N/A	N/A	N/A
AE100s6	TGTGTGTGCATGAGTGTAGGTG	1081	CTTTGTCATTTCCATACCTGTGAAA	1169	ACCTTCATAGAGGGTATAATAAAAG	1257
AE100s7	ATCCAGTAATGGCAAAGCCAG	1082	GTCAGCCTTAGGGTAACAGTTTTG	1170	AAGAGTTTGTTTGAGGAAAGGGTTT	1258
AE100s8	GCAAATCTCACGTCTGCTG	1083	CAGGTCTGGGGGCACAGTA	1171	GTAAAGGAGGTCTCNATNGCACAGGGG	1259
AE100s9	AAAACTAGGAAAGACAGAAAGCACAC	1084	TTTCAGAGGACTGGCAGGAG	1172	CACAGAGTAGAGAGNATTGCCACGAAA	1260
AE103s1	AACTTCTTTGCCTTCACTAACAGCT	1085	GATGAAGATATTGGAGCAAGACTTTTAG	1173	CCAGTAATTTATGTCTTTGTGGGCC	1261
AE103s10	N/A	N/A	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGAATGTTACCAAATT	1086	GACTCTGAGCCTCCTGCCTC	1174	ATCCTGAATTATCCAAGTGGGCCCT	1262
AE103s12	N/A	N/A	N/A	N/A	N/A	N/A
AE103s13	CCACCGAGTTTCTGGTAATTTG	1087	CTTTGAATAGACAAATGGAAGTGTARTAAGA	1175	CAGCAGGAAACAAATAACAAGTATC	1263
AE103s14	TGTCATAGCAGCAGCAGGAA	1088	CCTGGCAGTTAGCCTAGAAAGC	1176	ACAAGTATCRGGTAATGNCCTCTCTTA	1264
AE103s2	TGACAATGCTCCAGAAGCC	1089	CAACAGGACAAAAAGGTTCCC	1177	CTGGGACCTGCTGNACAGAGTGCTGCC	1265
AE103s3	ACTTTTCTGGCGGAATTAAAACA	1090	ACCCCCCAATCTACGGGA	1178	TGAACCAANANGCTTGGCTTTCTTATC	1266
AE103s4	N/A	N/A	N/A	N/A	N/A	N/A
AE103s5	N/A	N/A	N/A	N/A	N/A	N/A
AE103s6	TTCTGGGCAGAGAATATCTGGA	1091	CCACCAGGAAGATGCTGATG	1179	GAGCCCTCCTCTGCCGTGTCATCAA	1267
AE103s7	N/A	N/A	N/A	N/A	N/A	N/A
AE103s8	ATCTGAACATCACCGCCT	1092	GTAGTTGAAGAAGACGATCGC	1180	AGATCTGAACATCACCGCCTGCATC	1268
AE103s9	N/A	N/A	N/A	N/A	N/A	N/A
AE104s1	GAGAGCAATAAATGTCTGTTTTTTGATAA	1093	CTCACCTGTGCTGCTTGTG	1181	CACTGGGCAAATCNGCNGGGCTCCCCC	1269
AE104s10	GGTTGGGGCCTCAGGGTG	1094	GTGGCGGTGTGAAGCACC	1182	GTNGGAATGACAGGTNGAAGGGAGCCA	1270

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPIT	ORCHID_SNPIT (SEQ ID NO:)
AE104s11	TTGGATGTGAAATGCTTCCTG	1095	GCCCTATGCATGGTGTAGATG	1183	TTACAACATAACAGCNCATTGAGTCTT	1271
AE104s12	ATTTTCTCGTTTGGATGTGAAATG	1096	CGGCCCTATGCATGGTGTA	1184	TAACAGCTCATTGAGTCTTKCACAG	1272
AE104s13	GCCATTGCGGCAGAGCTC	1097	AAAAAAAGAGGCTGTGTTTTGTCA	1185	GGGCAGTCATTCAGCACCAGAGCAC	1273
AE104s14	AAGTGAATGAGTGCTGCCCT	1098	AAGGTGGCCCAGTATGAGC	1186	CCCTAGAAGAGTGTGAAAAGGAATG	1274
AE104s16	GATGCATGGATGGAGGAGG	1099	CAGTGATGGGGAATTCATTATCC	1187	ATTCCTTCACTCATNTATNAAACAAAA	1275
AE104s17	GATGGAACAGATGAAGGAGAGG	1100	CATAAATGCCCCTCCTCCAT	1188	TACGTTGAGCGATGAGCCCCAGGTT	1276
AE104s18	AGAAGAAAAGATGGTTAGATGGCA	1101	CATTGAGTCAGGGACTCAGCA	1189	ACAGGGGCTGGGGATNGCNAAATACAC	1277
AE104s19	TAACTAGTGAACTGAGGAATCCCTTT	1102	CACTCTGAGTCCAAATGTTCTCTC	1190	GTGGTGGGCACGGAGTCCTCAC	1278
AE104s2	GAGAGCAATAAATGTCTGTTTTTTGATAA	1103	CTCACCTGTGCTGCTTGTG	1191	GTCAGGGAGGGGCNCACCTGGGCGCGG	1279
AE104s20	TTTACACTCCCAGGGCTGAG	1104	CTCTTCCCCAGATCCACTGG	1192	TTTTTGNAGCCTTAAAACCCTTCCTTC	1280
AE104s21	GGATTTCTTTGTAYGCCACGTAC	1105	CATACATCTCCGAAGAAACGG	1193	GCAGAAGCTGTCCTGTTTCCTGGGT	1281
AE104s22	N/A	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGGAGTGGCGGCG	1106	GCAGGAGTGCAGAGCTCAG	1194	GAAGTGCCCAGGAGGCTGNTGACATCA	1282
AE104s24	N/A	N/A	N/A	N/A	N/A	N/A
AE104s25	N/A	N/A	N/A	N/A	N/A	N/A
AE104s26	TGAATAGATTAAAGAAACCCAGGG	1107	GTTCTCCGTCCCTGCCCC	1195	CATTGCACCAAANCTGGATGGC	1283
AE104s27	TCGACCGTCTCGTCGAAC	1108	GAAAGAGAAGGAGCCATCTCCA	1196	GCTTTCNGGTGGTGNCAGTGCCCAGTC	1284
AE104s28	N/A	N/A	N/A	N/A	N/A	N/A
AE104s29	N/A	N/A	N/A	N/A	N/A	N/A
AE104s3	TTTGCAAGGGAGGGAATC	1109	CAACCCTGCACTCCAAGC	1197	GAGCGAAGGGCTGGCTGAGGTCATG	1285
AE104s30	N/A	N/A	N/A	N/A	N/A	N/A
AE104s31	N/A	N/A	N/A	N/A	N/A	N/A
AE104s32	N/A	N/A	N/A	N/A	N/A	N/A
AE104s33	TAGGGATACAATGGCTAGGAGCT	1110	GTTTGGGACCCCATGTTCTAT	1198	ACCTTTTGCTTGATTTTTCACTGTA	1286
AE104s34	ACACTGGTGCTTCACACCG	1111	GTACATGTGAGGCATCWTTACGC	1199	GGCTCCCAATACTGATTCTGCTCCA	1287
AE104s35	N/A	N/A	N/A	N/A	N/A	N/A
AE104s36	CCCTTCTGCTGTCCATATCA	1112	CATCTTGAAGGAACTCAAAGACTCA	1200	ACCCACAGCACCCTGCTNGACCGTCTC	1288
AE104s4	AGTGAGAGGCTTGGAGTGCA	1113	CTTTGGATGAAAAAGAGGAAGCA	1201	AGGGTTGCAGGGAGANCTGGGATGAGG	1289
AE104s5	TGCAGGGTTGCAGGGAGA	1114	CAAGAGAAGGCGTCTTTGGAT	1202	GCTGGGATGANGYCTGGGGTGCTGCCT	1290
AE104s6	GGCTCACAACTGTGGAATGTC	1115	CAAAGAGGCCCTGCCCGA	1203	GTTCTCTGGAGAAAAAACTGTGCTG	1291
AE104s7	AACTGTGGCCCAGAGGGT	1116	AACCCCTTACCCACCAGC	1204	CCCCCTCTCCAAGTCTNTGTCCCACAA	1292
AE104s8	ATGTACGTAGCACCCTTTGCTTT	1117	GGAGACCAAGGTTCCAGCTC	1205	GAAGAGGGAACTGAGGCAGGGACAG	1293
AE104s9	TATTTCTAGACCTCAGTGTCTTTTCCTTATAG	1118	GAAGTCGTTGTGAGGGTTAAAGG	1206	AAGGGTGCTACGTANATNTGAGGCATC	1294
AE105s1	GAGAGGACTCTGAAGGGGG	1119	AGGTCTTCACCTGCTCTGCA	1207	CCCAGCGCTGGGGAAAGAAAGGACA	1295
AE105s2	ATTGTGACAGAGGGTGGGG	1120	CAAACTCAGATTGTGGGAGAGC	1208	GAGATGCGGTAGGAAGACTGTTAAG	1296
AE105s3	N/A	N/A	N/A	N/A	N/A	N/A
AE105s4	GCGAAGGGAAGGTCGCAA	1121	TTGAGTTGGTTGTCGGCAA	1209	AAGCTGGAANCCTCNAGGATGGGTTCA	1297
AE105s5	TGTTGGGGGATGCTTTGG	1122	GATGCTGAATGGGGAAAAGG	1210	AAGCTCTACCACGCCTTCTCAG	1298
AE105s6	ATCTCTGTGGCCCGCACC	1123	CATATACTCGCCCCATGAAGAC	1211	GGAACTTGTNCTNCTGGTCCCAGAGCA	1299
AE106s1	TATCAAAGGCCACAGCCG	1124	CACAACGAATGGTACTACGGC	1212	TACTGGCGAAGACAGCGGCGATGGG	1300
AE106s2	ATGGTCTCTGTGGTTGAGTAGTAGC	1125	CATCATACATCCCCTCCAGC	1213	CCAGCAGGAGAGCCAGGACCCA	1301
AE106s3	ATACCTGGGGATATTTTGTGC	1126	CTACCACGAGCAAGTCTCTG	1214	CCAAGCGCAAGGTGAGCAGGGG	1302
AE106s4	TGCAGAATTCATCCTGAAATGA	1127	CTGTKTGACTCAAACCAAATCACT	1215	AGGTCGGACCANCTTTTCCCAA	1303
AE106s5	AAAAGCTGGTCCGACCTTTTATT	1128	TCAAAAAATCTCAATTCTTCCCTATCT	1216	TCCCTATCTTTGCNACNCTNATGCTGT	1304
AE106s6	TTTGAGTCAMACAGCATGAGG	1129	CATGGAAATTCCCTTCATCTG	1217	ACCCATACTGACCCTTTTNGCAAGTCC	1305
AE106s7	ATGGTCTTGGAGTCACTTCGTG	1130	CCCACGAGGAGGAGCCAG	1218	AGAGCAGTTNGAGGTCAGGTNCAGGGA	1306

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPIT	ORCHID_SNPIT (SEQ ID NO:)
AE106s8	N/A	N/A	N/A	N/A	N/A	N/A
AE106s9	N/A	N/A	N/A	N/A	N/A	N/A
AE107s1	GTTCGTAGTCTCATTTCCAGATGATC	1131	ACACACAGCATGAAGTCTGTCAC	1219	CAAAATCCTGCCTAATGATGAGTGC	1307
AE107s2	AGCATCGAACCAGAGAATTGTATG	1132	CTTCCCTGGCCCTTTCTC	1220	TCCCTTGNACRCAGGAGTCCCCATCCC	1308
AE107s3	CCTGCTGATACCATCACAGATG	1133	CATACAATTCTCTGGTTCGATGC	1221	GCTGTGAAGNTCGNGGAGTTGCCCACC	1309
AE107s4	ATCGAACCAGAGAATTGTATGTGG	1134	GGGAGAAAAAGGGCTGCA	1222	AAGGCRGGGATGGGGACTCCTG	1310
AE107s5	ACCTGGACCCACTCGGCT	1135	CCTTTCCCCACCTGCTGG	1223	TGNGGCCACCCCAGCTGTGTCA	1311
AE107s6	CCAGTAAAATCAAATGTGCATCC	1136	CAGCCTCAGCCGAGTGGG	1224	ATGTGTGTCACGTTCTGCCATCACC	1312
AE109s1	AATAGCTTATCCAATAAGGAATAGGTTACTTT	1137	GAATTGATTATTTTTGAGTGCACAGTC	1225	ATCTGGAACTTATAGTNTTGAAAAGAA	1313
AE109s2	GGGGGTTCAGGGCCTTTT	1138	GCAAATTTAGCCAAGTCAAAGAGA	1226	GAGGGGTTCCAGANGTACNTATATTTA	1314
AE109s3	TGGGGCCAAAGGAGACTAG	1139	GCTGAAAGACCAGAACAAGAATTC	1227	AAGTAGACAAGGAATGGGTGTGAAA	1315
AE109s4	GTGTTGAAACACACATATCTGCAAT	1140	TGGAAAAGTTTGTAACCCAGATAATC	1228	TCATAATCACNANTNAAANTTAGTAGC	1316
AE109s5	GTGTTCAACTGCAAATTAAAGATAATAAACA	1141	ACATGGCAAAGAAGTAAATTGCTG	1229	GAAATTTTGCTGAAGAGAATGCTAA	1317
AE109s6	AACTCAAATCAAGATTATTCCCCTG	1142	GTTACCAAATACAACAACAATAACCAGTATT	1230	CACATGTAAATGACTCAGAATAATG	1318
AE109s7	CCCTCACCCTTAGATGAAAGTAAAA	1143	TTTGAAACCAAGAATCTCCTTTAATTT	1231	TTCAGTTCTAGGAATNATATCAGACAC	1319
AE109s8	N/A	N/A	N/A	N/A	N/A	N/A
AE109s9	AGGCTCACTCAAAAAGGCAATT	1144	TGCCTCCCTGCTCATTTG	1232	CTTGGTAANAAGCCCCATNAATTCTTC	1320
AE110s1	N/A	N/A	N/A	N/A	N/A	N/A
AE110s10	CACCTTGGACGTGGATGAG	1145	ATGTGGCGATTGGTCTGG	1233	GGNTGGCACCGAGGNTGCAGCAGCCAC	1321
AE110s11	CACCTCCTGCACACTCTCA	1146	CATGGTGTCATTCAGGAATTTTG	1234	AACCTCNCCGGNCATGGGCTGGAAACA	1322
AE110s12	AGATTTGGGGGAGAAACTGG	1147	CAGTAGAACTGGTCTTTGTATTGTTACC	1235	TNTCTTGGACAGATGTTNATTATGAAA	1323
AE110s2	CTGTACCTTCTTTTCATCTTCCCTT	1148	GCAGCATCATGGGCACCC	1236	CCGGACTGNTGTGTTCTCATCAACATA	1324
AE110s3	AAGGAGGGCTCTGCCCAG	1149	GATGCAACTCTAGCTTCTTGTAAAAATT	1237	GATCCTGGCTTGTTCANTANTCTAATG	1325
AE110s4	N/A	N/A	N/A	N/A	N/A	N/A
AE110s5	CTTATCAACGACCACGTCAAGAA	1150	GATTTAGCATATACCAATGATCTGACTCT	1238	GAGGGAAGATTGTGGATTTGGTCAG	1326
AE110s6	GTCAAACTAAATGGCTGAAAGTGG	1151	TTTCAGATGAGTTGATTTCATTAGTGC	1239	AGACCCTAAAATAAACTCTGAGGAT	1327
AE110s7	AGGGTCAAACTAAATGGCTGAAA	1152	CACTTGTCTTTCAGATGAGTTGATTTC	1240	TAAACCATATAAAGCACTCCACAGA	1328
AE110s8	AGAAACTGGAGTATCCTTTCTTGGA	1153	CTGTAGAGGTCAGTAGAACTGGTCTTTG	1241	TATGAAACGNGTACCANTTCTATCCCC	1329
AE110s9	N/A	N/A	N/A	N/A	N/A	N/A

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SNP_ID	GBS_LEFT	GBS_LEFT (SEQ ID NO:)	GBS_RIGHT	GBS_RIGHT (SEQ ID NO:)
AE100s1	TGTAAAACGACGGCCAGTAGTTCCTCCTCCTCCCTCACT	1330	CAGGAAACAGCTATGACCAGAAGCTCTGGGGTCTCTGAT	1451
AE100s10	TGTAAAACGACGGCCAGTGGCATTCACAGGTGATTCAGT	1331	CAGGAAACAGCTATGACCCACCAGGCAAGCAAATCATAT	1452
AE100s11	TGTAAAACGACGGCCAGTTTCTGGGCTTTACCCTCTCTC	1332	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACATCCA	1453
AE100s12	TGTAAAACGACGGCCAGTTTCTGGGCTTTACCCTCTCTC	1333	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACATCCA	1454
AE100s13	TGTAAAACGACGGCCAGTCCAGGTGCAGGATTAACAGAC	1334	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACATCCA	1455
AE100s14	TGTAAAACGACGGCCAGTACTAGGAACTTGCACAGTCCG	1335	CAGGAAACAGCTATGACCATGCACATACCACAGAGGAGG	1456
AE100s15	TGTAAAACGACGGCCAGTCCTCACACCCTATCCTACACG	1336	CAGGAAACAGCTATGACCATGCACATACCACAGAGGAGG	1457
AE100s16	TGTAAAACGACGGCCAGTCAGTGAGATCTTGCCACTGC	1337	CAGGAAACAGCTATGACCCAAGCTAAGGAAAAGCCATACC	1458
AE100s17	TGTAAAACGACGGCCAGTCAGGCAGACAATGATGTGATG	1338	CAGGAAACAGCTATGACCTGTGCTCCTCTGAAGTCTGGT	1459
AE100s18	TGTAAAACGACGGCCAGTTATCCAGGTATGGTGGCATGT	1339	CAGGAAACAGCTATGACCATAGCGATGTTGTTGGACTGG	1460
AE100s19	TGTAAAACGACGGCCAGTCAGAGGGAAGCACGTGATG	1340	CAGGAAACAGCTATGACCACTGGTTTCTGAAACCCACCT	1461
AE100s2	TGTAAAACGACGGCCAGTTGTAAAGCCCTTTGCAGAAGT	1341	CAGGAAACAGCTATGACCCTTGTCAGCTACAAGCCCAAG	1462
AE100s20	TGTAAAACGACGGCCAGTCTCTGAAAAGCCCCAGAGAAT	1342	CAGGAAACAGCTATGACCCTGTTGAAGCCACTCGAACTC	1463
AE100s21	TGTAAAACGACGGCCAGTGAGGCTCCAGACTCTCCTGTT	1343	CAGGAAACAGCTATGACCGGAGCAGCTGTAGCAGTCTGT	1464
AE100s22	TGTAAAACGACGGCCAGTCATTGCCTAGAAACCTTTGCA	1344	CAGGAAACAGCTATGACCATTGCTCTCTTGGGGTTTTGT	1465
AE100s23	TGTAAAACGACGGCCAGTAGCCACAGCTACAATGCTGTT	1345	CAGGAAACAGCTATGACCAAAACCCAGAGGCAAGTGTCT	1466
AE100s24	TGTAAAACGACGGCCAGTCTGCCGTCAACACAGAACTCT	1346	CAGGAAACAGCTATGACCGAACTTGTCCACGATCTCTGC	1467
AE100s25	TGTAAAACGACGGCCAGTAGAAGAACAGTTCTCCTCCGG	1347	CAGGAAACAGCTATGACCCCATGTGAACTCGTGAGCTTT	1468
AE100s26	TGTAAAACGACGGCCAGTCATGCCTTGCCTTGTACTTTC	1348	CAGGAAACAGCTATGACCGGCAACTCCCTACTCCACACT	1469
AE100s27	TGTAAAACGACGGCCAGTATGGAACACAGAGGGGTTAGG	1349	CAGGAAACAGCTATGACCGTCTGCAAATCCACACTCACA	1470
AE100s28	TGTAAAACGACGGCCAGTGGGTTGTATACCACACCCTGG	1350	CAGGAAACAGCTATGACCACAGCCAAATTCCTATGGCTT	1471
AE100s29	TGTAAAACGACGGCCAGTCGAGATAGGAAAGCCAGCTAG	1351	CAGGAAACAGCTATGACCGTTCTCCAACCTCTGGTAGGG	1472
AE100s3	TGTAAAACGACGGCCAGTCACTTGTGGAAAGCACACAGA	1352	CAGGAAACAGCTATGACCTGTCAGTGGCCTGAAATATCC	1473
AE100s30	TGTAAAACGACGGCCAGTAGGAAATTTGAGGCCATCACT	1353	CAGGAAACAGCTATGACCCCTCCTTCTACCAAGGTCCAT	1474
AE100s4	TGTAAAACGACGGCCAGTAGCAGTCAAGATCCCTTCCAT	1354	CAGGAAACAGCTATGACCGTTTCCTGAACACCTCTGGCT	1475
AE100s5	TGTAAAACGACGGCCAGTGAAAGAGCCCTCCCTCTCTC	1355	CAGGAAACAGCTATGACCTTGCAATGCGGTAGTCTTAAA	1476
AE100s6	TGTAAAACGACGGCCAGTCAAGGTGGACAGTCTTCGGTA	1356	CAGGAAACAGCTATGACCCTGCTGGCATTCCTCACTTAC	1477
AE100s7	TGTAAAACGACGGCCAGTTCCTCATAGCAGCCCTATTGA	1357	CAGGAAACAGCTATGACCGGACGCCAGATACTTTCTCCT	1478
AE100s8	TGTAAAACGACGGCCAGTATCCGAAGACAGGGAGTTCAT	1358	CAGGAAACAGCTATGACCCTGTTCTTCACTGCCTTGGTC	1479
AE100s9	TGTAAAACGACGGCCAGTATCCGAAGACAGGGAGTTCAT	1359	CAGGAAACAGCTATGACCTGGGGAGTAGGTGTCTGTCAC	1480
AE103s1	TGTAAAACGACGGCCAGTTCTTTGCCTTCCTGGAATTCT	1360	CAGGAAACAGCTATGACCTCAATGCTGTTTTAATTCCGC	1481
AE103s10	TGTAAAACGACGGCCAGTCGTCCCAGATCTGAACATCAC	1361	CAGGAAACAGCTATGACCGACTGCTTGCACCTGGAATAA	1482
AE103s11	TGTAAAACGACGGCCAGTGAACCAAGAAGCTTGGCTTTC	1362	CAGGAAACAGCTATGACCCTAAATCTGTTTCCCTGGGCT	1483
AE103s12	TGTAAAACGACGGCCAGTAACTTCCCAGACTCAAGGGAT	1363	CAGGAAACAGCTATGACCTCCCTGTATTCCTGGCAGTTA	1484
AE103s13	TGTAAAACGACGGCCAGTCAAGTGATCCTCCACTTTGGT	1364	CAGGAAACAGCTATGACCTGGTGTGTTCATGCAATTTCT	1485
AE103s14	TGTAAAACGACGGCCAGTCCTCCACTTTGGTCTCCCATA	1365	CAGGAAACAGCTATGACCTGGTGTGTTCATGCAATTTCT	1486
AE103s2	TGTAAAACGACGGCCAGTGCTGTAGTCTGCCACTTCCTG	1366	CAGGAAACAGCTATGACCGATATTCTCTGCCCAGAAGGG	1487
AE103s3	TGTAAAACGACGGCCAGTAGGACCAAGGTCTGGGAACT	1367	CAGGAAACAGCTATGACCCTGAATTCCTCTGGCCTCTG	1488
AE103s4	TGTAAAACGACGGCCAGTGCCTGGAACACAGACCATTAA	1368	CAGGAAACAGCTATGACCAAGGCAGATGGATCAGATGAA	1489
AE103s5	TGTAAAACGACGGCCAGTAACTTCCCAGACTCAAGGGAT	1369	CAGGAAACAGCTATGACCTCCCTGTATTCCTGGCAGTTA	1490
AE103s6	TGTAAAACGACGGCCAGTCCCTTCTGGGCAGAGAATATC	1370	CAGGAAACAGCTATGACCAGTGGTAGGAGGAAACCCAGA	1491
AE103s7	TGTAAAACGACGGCCAGTCCCTTCTGGGCAGAGAATATC	1371	CAGGAAACAGCTATGACCAGTGGTAGGAGGAAACCCAGA	1492
AE103s8	TGTAAAACGACGGCCAGTGCATCTTCCTGGTGGTGG	1372	CAGGAAACAGCTATGACCCTGTGGTCTTGCTATCCTTCG	1493
AE103s9	TGTAAAACGACGGCCAGTCGTCCCAGATCTGAACATCAC	1373	CAGGAAACAGCTATGACCAGAATTCCAGGAAGGCAAAGA	1494
AE104s1	TGTAAAACGACGGCCAGTGTGGTCTTTAAAGGAGGCCTG	1374	CAGGAAACAGCTATGACCGACTTTTGCACCAACCGAATA	1495
AE104s10	TGTAAAACGACGGCCAGTGGTCTCAGCACTGTGATCCTC	1375	CAGGAAACAGCTATGACCGTGCTACGTACATGTGAGGCA	1496

Table XI (2 of 3)

SNP_ID	GBS_LEFT	GBS_LEFT (SEQ ID NO:)	GBS_RIGHT	GBS_RIGHT (SEQ ID NO:)
AE104s11	TGTAAAACGACGGCCAGTTCGGGAGTTGTAACAAATGCT	1376	CAGGAAACAGCTATGACCGAGGCTGTGTTTTGTCACACA	1497
AE104s12	TGTAAAACGACGGCCAGTGCTATGCAAAAACCTCATCCA	1377	CAGGAAACAGCTATGACCGAGGCTGTGTTTTGTCACACA	1498
AE104s13	TGTAAAACGACGGCCAGTCATCTACACCATGCATAGGGC	1378	CAGGAAACAGCTATGACCTGGAGGAAGAAAACAGGTGAA	1499
AE104s14	TGTAAAACGACGGCCAGTTAGCCTCTCCAGTTCTAGCCC	1379	CAGGAAACAGCTATGACCATTTCTAATCGGTCTTGCCCA	1500
AE104s16	TGTAAAACGACGGCCAGTAATAAAAGAGGTGCTGACCCAC	1380	CAGGAAACAGCTATGACCCTAGAATCATAGGCGCAGCAG	1501
AE104s17	TGTAAAACGACGGCCAGTCCACCATGACCCAAGTTTAT	1381	CAGGAAACAGCTATGACCGCCACTTGTTTCATACTCCCA	1502
AE104s18	TGTAAAACGACGGCCAGTGAGGAATCCCTTTGACTCACC	1382	CAGGAAACAGCTATGACCGACTGAGCAATGTCTGGCTTC	1503
AE104s19	TGTAAAACGACGGCCAGTTGGTTCCTTCAACTGTTGTCC	1383	CAGGAAACAGCTATGACCACAAACGTCCATTGAGTCAGG	1504
AE104s2	TGTAAAACGACGGCCAGTGTGGTCTTTAAAGGAGGCCTG	1384	CAGGAAACAGCTATGACCGACTTTTGCACCAACCGAATA	1505
AE104s20	TGTAAAACGACGGCCAGTAGATGTATGGCGGAGGTTTCT	1385	CAGGAAACAGCTATGACCGCCACCCATAAACTGATCTGA	1506
AE104s21	TGTAAAACGACGGCCAGTTTTTGGATGTAAACAGTGGGC	1386	CAGGAAACAGCTATGACCAATGTTTTGAAAGTCCCTGCC	1507
AE104s22	TGTAAAACGACGGCCAGTGGAAGCCCCATGTGAATAAAT	1387	CAGGAAACAGCTATGACCTTGAGCAAAACTGAGAAAGCC	1508
AE104s23	TGTAAAACGACGGCCAGTACTTCAGTCGCTCCCTGGTAC	1388	CAGGAAACAGCTATGACCACATGGAAATCTTCGCAAGAG	1509
AE104s24	TGTAAAACGACGGCCAGTTCTCCATCTGAATGGGTTCTG	1389	CAGGAAACAGCTATGACCACGAGATGCAGAAGTTCAAGG	1510
AE104s25	TGTAAAACGACGGCCAGTAAGCAACTGTCCCTCAATCCT	1390	CAGGAAACAGCTATGACCTAATCACACAGATCGCCTCCT	1511
AE104s26	TGTAAAACGACGGCCAGTGACCTCCTTGTCCATCAGTGA	1391	CAGGAAACAGCTATGACCCCAAGGACTCCAAAATCACAA	1512
AE104s27	TGTAAAACGACGGCCAGTCCCTCACAACGACTTCATGTT	1392	CAGGAAACAGCTATGACCTCACTGATGGACAAGGAGGTC	1513
AE104s28	TGTAAAACGACGGCCAGTTTCTCTCCAAATGCTCCTGTG	1393	CAGGAAACAGCTATGACCGGGTGATATGGACAGCAGAAG	1514
AE104s29	TGTAAAACGACGGCCAGTGGTCTCAGCACTGTGATCCTC	1394	CAGGAAACAGCTATGACCGTGCTACGTACATGTGAGGCA	1515
AE104s3	TGTAAAACGACGGCCAGTGCAGGCAAATACCACTTTCAA	1395	CAGGAAACAGCTATGACCTTGGATGAAAAAGAGGAAGCA	1516
AE104s30	TGTAAAACGACGGCCAGTCCCAATACTGATTCTGCTCCA	1396	CAGGAAACAGCTATGACCGGAACTCAAAGACTCAAGTGGG	1517
AE104s31	TGTAAAACGACGGCCAGTTGGTTCCTTCAACTGTTGTCC	1397	CAGGAAACAGCTATGACCTTGAGTCAGGGACTCAGCAGT	1518
AE104s32	TGTAAAACGACGGCCAGTCCTGACTCAATGGACGTTTGT	1398	CAGGAAACAGCTATGACCAATCCATATTCACACCAAGCG	1519
AE104s33	TGTAAAACGACGGCCAGTCCTGACTCAATGGACGTTTGT	1399	CAGGAAACAGCTATGACCAATCCATATTCACACCAAGCG	1520
AE104s34	TGTAAAACGACGGCCAGTATCTTCCTCTGCCTCATCACA	1400	CAGGAAACAGCTATGACCTATTGCACAACCATCTGTCCC	1521
AE104s35	TGTAAAACGACGGCCAGTTCAGACTTTGAAGACATGGCC	1401	CAGGAAACAGCTATGACCTATTGCACAACCATCTGTCCC	1522
AE104s36	TGTAAAACGACGGCCAGTTGTACGTAGCACCCTTTGCTT	1402	CAGGAAACAGCTATGACCTCACTGATGGACAAGGAGGTC	1523
AE104s4	TGTAAAACGACGGCCAGTGAATCCCAAAGAGATTGAGGC	1403	CAGGAAACAGCTATGACCACAAGCTTGGAGGAAGCATTT	1524
AE104s5	TGTAAAACGACGGCCAGTGAATCCCAAAGAGATTGAGGC	1404	CAGGAAACAGCTATGACCGACATTCCACAGTTGTGAGCC	1525
AE104s6	TGTAAAACGACGGCCAGTTGCTTCCTCTTTTTCATCCAA	1405	CAGGAAACAGCTATGACCCAGCCTACAGGAAGTGGGAG	1526
AE104s7	TGTAAAACGACGGCCAGTGGACCCACAAATCAATGCTT	1406	CAGGAAACAGCTATGACCATACCAACAGCTTCCCCAGTT	1527
AE104s8	TGTAAAACGACGGCCAGTTGCTCCACGGAGCTATTTCTA	1407	CAGGAAACAGCTATGACCCAAAGACTCAAGTGGGAACGA	1528
AE104s9	TGTAAAACGACGGCCAGTGTGGGAATGACAGGTGGAAG	1408	CAGGAAACAGCTATGACCGGGTGATATGGACAGCAGAAG	1529
AE105s1	TGTAAAACGACGGCCAGTAGAGCATCCTCTCTTACCCCA	1409	CAGGAAACAGCTATGACCACTGTACCTGCCCGGTTATTT	1530
AE105s2	TGTAAAACGACGGCCAGTAAGCCTGGAAGCTTAGGTCTG	1410	CAGGAAACAGCTATGACCTTTGATGCGGGGTAGTGTTAG	1531
AE105s3	TGTAAAACGACGGCCAGTTATTTTCTAGGTGGGGCAGCT	1411	CAGGAAACAGCTATGACCTACCCCTCTAACTTGCAGGGT	1532
AE105s4	TGTAAAACGACGGCCAGTGAACCACAGGATAGAGCCTCC	1412	CAGGAAACAGCTATGACCATCTGTTGGGAGCTGGGTAGT	1533
AE105s5	TGTAAAACGACGGCCAGTACTACCCAGCTCCCAACAGAT	1413	CAGGAAACAGCTATGACCTGGATTGGTGACTCTTATGGG	1534
AE105s6	TGTAAAACGACGGCCAGTGGACCCAGATCTTCAGGTTTC	1414	CAGGAAACAGCTATGACCAACTGAGAGCTGAGGCTGGA	1535
AE106s1	TGTAAAACGACGGCCAGTAGAGTGGCCAATCTTCCACTT	1415	CAGGAAACAGCTATGACCGTGGATCATCTTAGCCCACAA	1536
AE106s2	TGTAAAACGACGGCCAGTGGCATGGGGAGTCATCTCTAC	1416	CAGGAAACAGCTATGACCTGGCAGGAAAAATATGGAATC	1537
AE106s3	TGTAAAACGACGGCCAGTCAGATCTGGGTTCCAAAGACA	1417	CAGGAAACAGCTATGACCCTGATCTACTTCCTCCCCCTG	1538
AE106s4	TGTAAAACGACGGCCAGTCTTTTGTTCACCCTGTCAAGC	1418	CAGGAAACAGCTATGACCTTGCAAAAAGGGTCAGTATGG	1539
AE106s5	TGTAAAACGACGGCCAGTGGCTCCAGGAAAATGAGTCTT	1419	CAGGAAACAGCTATGACCTCTGGAACCATCAGAAACACC	1540
AE106s6	TGTAAAACGACGGCCAGTAAAAGCTGGTCCGACCTTTTA	1420	CAGGAAACAGCTATGACCTCCAACTGCTCTTCACGAAGT	1541
AE106s7	TGTAAAACGACGGCCAGTTGAGGGTGTTTCTGATGGTTC	1421	CAGGAAACAGCTATGACCATGAAATCCACCCGGTATCTC	1542

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SNP_ID	GBS_LEFT	GBS_LEFT (SEQ ID NO:)	GBS_RIGHT	GBS_RIGHT (SEQ ID NO:)
AE106s8	TGTAAAACGACGGCCAGTATGGATTTCTGGTTCCCTTTG	1422	CAGGAAACAGCTATGACCCTTCTTCCTCCTGCCCTACAT	1543
AE106s9	TGTAAAACGACGGCCAGTCTTTAAGAGCAAGCGAAGTGG	1423	CAGGAAACAGCTATGACCCACACTATGGGCCAGTGAGAT	1544
AE107s1	TGTAAAACGACGGCCAGTAATTGTATGTGGGGGCAGACT	1424	CAGGAAACAGCTATGACCGTGAAGCAGATGCCTGGTTAG	1545
AE107s2	TGTAAAACGACGGCCAGTCCTGACAGAGCCTGCTGATAC	1425	CAGGAAACAGCTATGACCATTTTGAGGTCCACACACTGG	1546
AE107s3	TGTAAAACGACGGCCAGTGCCCAGTTTGTTCATGTCAGT	1426	CAGGAAACAGCTATGACCGGAAATGAGACTACGAACCCG	1547
AE107s4	TGTAAAACGACGGCCAGTCCTGACAGAGCCTGCTGATAC	1427	CAGGAAACAGCTATGACCAAGTCTGTCACCTTCTGGACG	1548
AE107s5	TGTAAAACGACGGCCAGTCCCTACCCCCAGTAAAATCAA	1428	CAGGAAACAGCTATGACCACCTCTCAGCCTCAGACCTTC	1549
AE107s6	TGTAAAACGACGGCCAGTGCCGTCAGAGTGCTGTCTTAT	1429	CAGGAAACAGCTATGACCCTGTTTGTCTGCACCTGTCAC	1550
AE109s1	TGTAAAACGACGGCCAGTTGACGAGAGTCAATTGAAAGGA	1430	CAGGAAACAGCTATGACCATGCAGACCAAAGCATCAAAG	1551
AE109s2	TGTAAAACGACGGCCAGTCAAAGTAGTTGAGCAGTGGCC	1431	CAGGAAACAGCTATGACCGACCATACAACAATTGGGTGG	1552
AE109s3	TGTAAAACGACGGCCAGTAAATGGCAGCTGTCACCATAG	1432	CAGGAAACAGCTATGACCACATGAATGTAAGGCCACTGC	1553
AE109s4	TGTAAAACGACGGCCAGTTCTGCAGAGAAAATAAACCACTGA	1433	CAGGAAACAGCTATGACCTCTTCAGCAAAATTTCCATTGT	1554
AE109s5	TGTAAAACGACGGCCAGTGCATTCTTGTGGATTATCTGGG	1434	CAGGAAACAGCTATGACCTCGACAGTGGGGAAACTTAAC	1555
AE109s6	TGTAAAACGACGGCCAGTTTGCCCATAGTGGTAACTTGC	1435	CAGGAAACAGCTATGACCCGAGTGGCTAATTTGAAACCA	1556
AE109s7	TGTAAAACGACGGCCAGTGCACACAGGAAGAACACACAA	1436	CAGGAAACAGCTATGACCCTCCCCCATGTCTCTCTATCC	1557
AE109s8	TGTAAAACGACGGCCAGTGTGCATGCATCTGTGTGTGTT	1437	CAGGAAACAGCTATGACCACATGAATGTAAGGCCACTGC	1558
AE109s9	TGTAAAACGACGGCCAGTTGCTTTCAAAATGCGATTTCT	1438	CAGGAAACAGCTATGACCCTTTCTTCCTGGGCTTTTCAG	1559
AE110s1	TGTAAAACGACGGCCAGTCAGGCATGTCAGGTTTTGAAT	1439	CAGGAAACAGCTATGACCTTGTAATCCATCCGTAGCACC	1560
AE110s10	TGTAAAACGACGGCCAGTCTTGCTGTGTTATCCCCAAGA	1440	CAGGAAACAGCTATGACCCTCCTGCTTGGAACAGATGAG	1561
AE110s11	TGTAAAACGACGGCCAGTAAGAACATCTTTTTCTCCCCG	1441	CAGGAAACAGCTATGACCATCCACAATCTTCCCTCGAGT	1562
AE110s12	TGTAAAACGACGGCCAGTGCAGGTCATGGAAGTGGATTA	1442	CAGGAAACAGCTATGACCAGCCATTTAGTTTGACCCTCC	1563
AE110s2	TGTAAAACGACGGCCAGTGATCTGGAGCGACTGTTTCTG	1443	CAGGAAACAGCTATGACCTTTGCCTTGGTTAGGGAGAAT	1564
AE110s3	TGTAAAACGACGGCCAGTCTTTCAACATCCATTTGTGGG	1444	CAGGAAACAGCTATGACCTGACGACTTACTTTGGATGCC	1565
AE110s4	TGTAAAACGACGGCCAGTCACAGGAAGCAACCTCTGAAG	1445	CAGGAAACAGCTATGACCGGAGCCAGAAATGGAGAACTT	1566
AE110s5	TGTAAAACGACGGCCAGTCCTTGCAAAATTCCTGAATGA	1446	CAGGAAACAGCTATGACCAGGGTTGCTCAACCCTATCAG	1567
AE110s6	TGTAAAACGACGGCCAGTCCTTGTCTGTACGGGGTAACA	1447	CAGGAAACAGCTATGACCCCAACAGAGCAGGAAATGAAG	1568
AE110s7	TGTAAAACGACGGCCAGTAACGGGTACCAATTCTATCCC	1448	CAGGAAACAGCTATGACCCTAGCACATATCCCAGCCAGA	1569
AE110s8	TGTAAAACGACGGCCAGTGATTTTGGGTGGATAGAAGCC	1449	CAGGAAACAGCTATGACCGGTTTACAAACCACTTTCAGCC	1570
AE110s9	TGTAAAACGACGGCCAGTGAAGGGTGCATGCCTGTAGT	1450	CAGGAAACAGCTATGACCTAAGTGACCTGCCCAAAGTTG	1571

Table XII

Sample Description

Race	Cases			Controls			Total
	Angioedema	Angioedema-like	Total	Angioedema	Angioedema-like	Total	
Blacks	11	10	21	32	19	51	72
Caucasians	12	22	34	38	69	107	141
Other	0	1	1	0	1	1	2
Total	23	33	56	70	89	159	215

Table XIII

Candidate Angioedema Susceptibility Genes

Chromosome	Gene	Gene ID
14	Bradykinin B2 Receptor	BDKRB2
19	Tissue Kallikrein	KLK1
X	Aminopeptidase P (Membrane Bound)	XPNPEP2

Table XIV

Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events

Gene ID	SNP ID	Sample or Subgroup Scores Test		DF	Probability	Estimate Type	A,a[1]	Copies of Rare Allele	Odds Ratio (OR)[2]	OR Lower 95% CL	OR Upper 95% CL	p(a)[3]
BDKRB2	AE104s9	Caucasians	7.01	2	0.0300	Asymptotic	A,T	1	3.41	1.3238	8.7969	0.28
					0.0251	Exact			3.37	1.2261	10.2718	
KLK1	AE107s2	Blacks	7.50	2	0.0062	Asymptotic	C,T	1	5.64	1.4211	22.3807	0.09
					0.0062	Exact			5.64	1.2422	34.7611	
XPNPEP2	AE100s4	Caucasians	13.44	2	0.0009	Exact	C,T	2	14.95	1.9838	+INF	0.28
		Angioedema-like	11.39	2	0.0022	Exact		2	10.82	1.3105	+INF	0.22
		Overall	10.72	2	0.0047	Asymptotic		2	11.11	1.2687	97.2709	0.23

1 Most frequent (common) allele, least frequent (rare) allele.

2 The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.